

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 5 :
C12N 15/85, 15/65, 15/67
C12N 15/13

A2

(11) International Publication Number:

WO 94/11523

(43) International Publication Date:

26 May 1994 (26.05.94)

(21) International Application Number: PCT/US93/11221

(22) International Filing Date: 12 November 1993 (12.11.93)

(30) Priority data:
07/977,691

13 November 1992 (13.11.92) US

(71) Applicant: IDEC PHARMACEUTICALS CORPORATION [US/US]; 11011 Torreyana Road, San Diego, CA 92121-1104 (US).

(72) Inventor: REFF, Mitchell, E.; 4166 Combe Way, San Diego, CA 92122 (US).

(74) Agents: WEISS, Steven, M. et al.; Lyon & Lyon, 611 West Sixth Street, 34th floor, Los Angeles, CA 90017 (US).

(81) Designated States: AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

Without international search report and to be republished upon receipt of that report.

(54) Title: FULLY IMPAIRED CONSENSUS KOZAK SEQUENCES FOR MAMMALIAN EXPRESSION

Neomycin phosphotransferase gene

Cla I -3 +1

TCAE 5.2 TTGGGAGCTTGG ATCGAT CC A cc ATG Ctt
Met Val

ANEX 1 TTGGGAGCTTGG ATCGAT CC I cc ATG Ctt
Met Leu

ANEX 2 CCaGCATGgAGGA ATCGAT CC I cc ATG Ctt
Met Leu

-3 +1 (I)

Pyxx ATG Pyxx

(57) Abstract

Disclosed herein are fully impaired consensus Kozak sequences which are most typically used with dominant selectable markers of transcriptional cassettes which are a part of an expression vector. These vectors are most typically utilized in the expression of proteins in mammalian expression systems. As defined, disclosed and claimed herein, a "fully impaired consensus Kozak" comprises sequence (I), where: "x" is a nucleotide selected from the group consisting of adenine (A), guanine (G), cytosine (C) or thymine (T)/uracil (U); "Py" is a pyrimidine nucleotide, i.e. C or T; "ATG" is a codon encoding for the amino acid methionine, the so-called "start" codon; and -3 and +1 are directional reference points vis-à-vis ATG, i.e. -3 is meant to indicate three nucleotides upstream of ATG and +1 is meant to indicate one nucleotide downstream of ATG. Dominant selectable markers further comprising artificial intronic insertion regions are further disclosed.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AT	Austria	GB	United Kingdom	MR	Mauritania
AU	Australia	GE	Georgia	MW	Malawi
BB	Barbados	GN	Guinea	NE	Niger
BE	Belgium	GR	Greece	NL	Netherlands
BF	Burkina Faso	HU	Hungary	NO	Norway
BG	Bulgaria	IE	Ireland	NZ	New Zealand
BJ	Benin	IT	Italy	PL	Poland
BR	Brazil	JP	Japan	PT	Portugal
BY	Belarus	KE	Kenya	RO	Romania
CA	Canada	KG	Kyrgyzstan	RU	Russian Federation
CF	Central African Republic	KP	Democratic People's Republic of Korea	SD	Sudan
CG	Congo	KR	Republic of Korea	SE	Sweden
CH	Switzerland	KZ	Kazakhstan	SI	Slovenia
CI	Côte d'Ivoire	LJ	Liechtenstein	SK	Slovakia
CM	Cameroon	LK	Sri Lanka	SN	Senegal
CN	China	LU	Luxembourg	TD	Chad
CS	Czechoslovakia	LV	Latvia	TC	Togo
CZ	Czech Republic	MC	Monaco	TJ	Tajikistan
DE	Germany	MD	Republic of Moldova	TT	Trinidad and Tobago
DK	Denmark	MG	Madagascar	UA	Ukraine
ES	Spain	ML	Mali	US	United States of America
FI	Finland	MN	Mongolia	UZ	Uzbekistan
FR	France			VN	Viet Nam
GA	Gabon				

FULLY IMPAIRED CONSENSUS KOZAC SEQUENCES FOR MAMMALIAN
EXPRESSION

5

37 C.F.R. §1.74(d)/(e) Copyright Notice

A portion of the disclosure of this patent document contains material which is
10 subject to copyright protection. The copyright owner does not object to the
reproduction by anyone of the patent document or the patent disclosure, as it
appears in the Patent and Trademark Office patent files or records, but
otherwise reserves all copyright rights whatsoever.

15

RELATED APPLICATIONS

This patent document is a Continuation-In-Part of U.S. Serial No. 07/977,691
filed November 13, 1992, pending. This patent document is related to
"THERAPEUTIC APPLICATION OF CHIMERIC ANTIBODY TO HUMAN B
LYMPHOCYTE RESTRICTED DIFFERENTIATION ANTIGEN FOR
20 TREATMENT OF B CELL LYMPHOMA," having U.S. Serial No. 07/978,891,
filed November 13, 1992 (pending), and "THERAPEUTIC APPLICATION OF
CHIMERIC AND RADIOLABELED ANTIBODIES TO HUMAN B
LYMPHOCYTE RESTRICTED DIFFERENTIATION ANTIGEN FOR
TREATMENT OF B CELL LYMPHOMA", having U.S. Serial No. _____, filed
25 simultaneously herewith. This patent document is related to commonly assigned
United States Serial No. 07/912,292 and entitled "RECOMBINANT
ANTIBODIES FOR HUMAN THERAPY," filed July 10, 1992. These documents
are incorporated herein by reference.

30

M I S S I N G P A G E

As noted, the advent of the biotechnology industry has allowed for the production of large quantities of proteins. Proteins are the essential constituents of all living cells and proteins are comprised of combinations of 20 naturally occurring amino acids; each amino acid molecule is defined ("encoded") by groupings ("codons") of three deoxyribonucleic acid ("DNA") molecules; a string of DNA molecules ("DNA macromolecule") provides, in essence, a blueprint for the production of specific sequences of amino acids specified by that blueprint. Intimately involved in this process is ribonucleic acid ("RNA"); three types of RNA (messenger RNA; transfer RNA; and ribosomal RNA) convert the information encoded by the DNA into, *eg* a protein. Thus, genetic information is generally transferred as follows: DNA → RNA → protein.

In accordance with a typical strategy involving recombinant DNA technology, a DNA sequence which encodes a desired protein material ("cDNA") is identified and either isolated from a natural source or synthetically produced. By manipulating this piece of genetic material, the ends thereof are tailored to be ligated, or "fit," into a section of a small circular molecule of double stranded DNA. This circular molecule is typically referred to as a "DNA expression vector," or simply a "vector." The combination of the vector and the genetic material can be referred to as a "plasmid" and the plasmid can be replicated in a prokaryotic host (*ie* bacterial in nature) as an autonomous circular DNA molecule as the prokaryotic host replicates. Thereafter, the circular DNA plasmid can be isolated and introduced into a eukaryotic host (*ie* mammalian in nature) and host cells which have incorporated the plasmid DNA are selected. While some plasmid vectors will replicate as an autonomous circular DNA molecule in mammalian cells, (*eg* plasmids comprising Epstein Barr virus ("EBV") and Bovine Papilloma virus ("BPV") based vectors), most plasmids including DNA vectors, and all plasmids including RNA retroviral vectors, are integrated into the cellular DNA such that when the cellular DNA of the

eukaryotic host cell replicates, the plasmid DNA will also replicate. Accordingly, as eukaryotic cells grow and divide, there is a corresponding increase in cells containing the integrated plasmid which leads to the production ("expression") of the protein material of interest. By subjecting the host cells
5 containing the plasmid to favorable growth conditions, significant amounts of the host, and hence the protein of interest, are produced. Typically, the Chinese Hamster Ovary ("CHO") cell line is utilized as a eukaryotic host cell, while *E. coli* is utilized as a prokaryotic host cell.

10 The vector plays a crucial role in the foregoing - manipulation of the vector can allow for variability as to where the cDNA is inserted, means for determining whether the cDNA was, in fact, properly inserted within the vector, the conditions under which expression of the genetic material will or will not occur, etc. However, most of the vector manipulations are geared toward a single
15 goal—increasing expression of a desired gene product, *ie* protein of interest. Stated again, most vector manipulation is conducted so that an "improved" vector will allow for production of a gene product at significantly higher levels when compared to a "non-improved" vector. Thus, while certain of the features/aspects/characteristics of one vector may appear to be similar to the
20 features/aspects/characteristics of another vector, it is often necessary to examine the result of the overall goal of the manipulation - improved production of a gene product of interest.

While one "improved" vector may comprise characteristics which are desirable
25 for one set of circumstances, these characteristics may not necessarily be desirable under other circumstances. However, one characteristic is desirable for all vectors: increased efficiency, *ie* the ability to increase the amount of protein of interest produced while at the same time decreasing the number of host cells to be screened which do not generate a sufficient amount of this protein. Such

increased efficiency would have several desirable advantages, including reducing manufacturing costs and decreasing the time spent by technicians in screening for viable colonies which are expressing the protein of interest. Accordingly, what would be desirable and what would significantly improve the state of the art are expression vectors with such efficiency characteristics.

SUMMARY OF THE INVENTION

The invention disclosed herein satisfies these and other needs. Disclosed herein are fully impaired consensus Kozak sequences which are most typically used with dominant selectable markers of transcriptional cassettes which are a part of an expression vector; preferably, the dominant selectable marker comprises either a natural intronic insertion region or artificial intronic insertion region, and at least one gene product of interest is encoded by DNA located within such insertion region.

As used herein, a "dominant selectable marker" is a gene sequence or protein encoded by that gene sequence; expression of the protein encoded by the dominant selectable marker assures that a host cell transfected with an expression vector which includes the dominant selectable marker will survive a selection process which would otherwise kill a host cell not containing this protein. As used herein, a "transcriptional cassette" is DNA encoding for a protein product (*eg* a dominant selectable marker) and the genetic elements necessary for production of the protein product in a host cell (*ie* promoter; transcription start site; polyadenylation region; etc.). These vectors are most preferably utilized in the expression of proteins in mammalian expression systems where integration of the vector into host cellular DNA occurs. Beneficially, the use of such fully impaired consensus Kozak sequences improves the efficiency of protein expression by significantly decreasing the number of

viable colonies while at the same time, significantly increasing the amount of
 protein expressed by such viable colonies. As used herein, a "natural intronic
 insertion region" is a region of DNA naturally present within a gene in this case,
 typically a dominant selectable marker, which can be utilized for insertion of
 5 DNA encoding a gene product of interest; an "artificial intronic insertion region"
 is a region of DNA which is selectively created in a gene (again, most typically, a
 dominant selectable marker) which can be utilized for insertion of DNA encoding
 a gene product of interest. Information regarding intronic positioning is
 described in Abrams, J.M. et al. "Intronic Positioning Maximizes Co-expression
 10 and Co-amplification of Nonselectable Heterologous Genes." *J. Bio. Chem.*,
 264:124:14016 (1989), and U.S. Patent No. 5,043,270 (both documents being
 incorporated herein by reference).

As defined, disclosed and claimed herein, a "fully impaired consensus Kozak"
 15 comprises the following sequence:

$$\begin{array}{ccc} -3 & & +1 \\ \text{Pyxx} & \text{ATG} & \text{Pyxx} \end{array}$$

20 where: "x" is a nucleotide selected from the group consisting of adenine (A),
 guanine (G), cytosine (C) or thymine (T)/uracil (U); "Py" is a pyrimidine
 nucleotide, i.e. C or T/U; "ATG" is a codon encoding for the amino acid
 methionine, the so-called "start" codon; and -3 and +1 are directional reference
 points vis-a-vis ATG, i.e. -3 is meant to indicate three nucleotides upstream of
 25 ATG and +1 is meant to indicate one nucleotide downstream of ATG.

Preferably, the fully impaired consensus Kozak is part of a methionine start
 codon that initiates translation of a dominant selectable marker portion of a
 transcriptional cassette which is part of an expression vector. Preferred
 30 dominant selectable markers include, but are not limited to: herpes simplex
 virus thymidine kinase; adenosine deaminase; asparagine synthetase;

Salmonella his D gene; xanthine guanine phosphoribosyl transferase; hygromycin B phosphotransferase; and neomycin phosphotransferase. Most preferably, the dominant selectable marker is neomycin phosphotransferase.

- 5 In particularly preferred embodiments of the invention, at least one out-of-frame start codon (*ie* ATG) is located upstream of the fully impaired consensus Kozak start codon, without an in-frame stop codon being located between the upstream start codon and the fully impaired consensus Kozak start codon. As used herein, the term "stop codon" is meant to indicate a codon which does not encode an
- 10 amino acid such that translation of the encoded material is terminated; this definition includes, in particular, the traditional stop codons TAA, TAG and TGA. As used herein, the terms "in-frame" and "out-of-frame" are relative to the fully impaired consensus Kozak start codon. By way of example, in the following sequence:

15

$$\text{GAC CAT GGC } \overset{-3}{\text{Cxx}} \overset{+1}{\text{ATG Cxx}}$$

- the underlined portion of the sequence is representative of a fully impaired
- 20 consensus Kozak (where "x" represents a nucleotide) and the codons GAC, CAT and GCC are "in-frame" codons relative to the ATG start codon. The above-lined nucleotides represent an "out-of-frame" start codon which is upstream of the fully impaired consensus Kozak start codon. Preferably, the out-of-frame start codon is within about 1000 nucleotides upstream of the fully impaired consensus
- 25 Kozak start codon, more preferably within about 350 nucleotides upstream of the fully impaired consensus Kozak start codon, and most preferably within about 50 nucleotides upstream of the fully impaired consensus Kozak start codon.
- Preferably, the out-of-frame start codon is a part of a consensus Kozak. By way of example, the sequence set forth above satisfies this criteria: the -5 nucleotide

is a purine (G); nucleotide -6, -7 and -8 encode an out- f-frame start codon (ATG); and nucleotide -11 is a purine (A).

5 Additionally, utilization of a fully impaired consensus Kozak within a secondary structure (ie a so-called "stem-loop" or "hairpin") is beneficially viable to impairment of translation of the protein encoded by the dominant selectable number. In such an embodiment, the start codon of the fully impaired consensus Kozak is most preferably located within the stem of a stem loop.

10 Particularly preferred expression vectors which incorporate these aspects of the invention disclosed herein are referred to as "TCAE," and "ANEX" and "NEOSPLA" vectors; particularly preferred vectors are referred to as ANEX 1, ANEX 2 and NEOSPLA3F.

15 These and other aspects of the invention disclosed herein will be delineated in further detail in the sections to follow.

BRIEF DESCRIPTION OF THE DRAWINGS

20 Figure 1 provides the relevant portion of a consensus Kozak and several particularly preferred fully impaired consensus Kozak sequences;

Figure 2 provides a diagrammatic representation of the vectors TCAE 5.2 and ANEX 1 (TCAE 12) designed for expression of mouse/human chimeric
25 immunoglobulin, where the immunoglobulin genes are arranged in a tandem configuration using neomycin phosphotransferase as the dominant selectable marker;

Figure 3 is a histogram comparing protein expression levels with the vectors TCAE 5.2 and ANEX 1;

5 Figure 4 provides a diagrammatic representation of the vector ANEX 2 designed for expression of mouse/human chimeric immunoglobulin, where the immunoglobulin genes are arranged in a tandem configuration using neomycin phosphotransferase as the dominant selectable marker;

10 Figure 5 is a histogram comparing protein expression levels with the vectors TCAE 5.2, ANEX 1 and ANEX 2;

Figure 6 provides a diagrammatic representation of a NEOSPLA vector designed for expression of mouse/human chimeric immunoglobulin; and

15 Figures 7A, 7B and 7C are histograms comparing protein expression levels with the vectors TCAE 5.2 vs. NEOSPLA 3F (7A). ANEX 2 vs. NEOSPLA3F (7B); and GK-NEOSPLA3F vs. NEOSPLA3F (7C).

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

20

Disclosed herein are nucleic acid sequence arrangements which impair translation and initiation of, most preferably, dominant selectable markers incorporated into mammalian expression vectors and which are preferably, but not necessarily, co-linked to an encoding sequence for a gene product of interest.

25 Preferably, the dominant selectable marker comprises at least one natural or artificial intronic insertion region, and at least one gene product of interest is encoded by DNA located within at least one such intron. Such arrangements have the effect of increasing expression efficiency of the gene product of interest by, *inter alia*, decreasing the number of viable colonies obtained from an

equivalent amount of plasmid DNA transfected per cell, while increasing the amount of gene product expressed in each clone.

5 For purpose of brevity and presentational efficiency, the focus of this section of the patent disclosure will be principally directed to a specific dominant selectable marker, neomycin phosphotransferase, which is incorporated into a mouse/human chimeric immunoglobulin expression vector. It is to be understood, however, that the invention disclosed herein is not intended, nor is it to be construed, as limited to these particular systems. To the contrary, the disclosed invention is applicable to mammalian expression systems *in toto*,
10 where vector DNA is integrated into host cellular DNA.

One of the most preferred methods utilized by those in the art for producing a mammalian cell line that produces a high level of a protein (*ie* "production cell
15 line") involves random integration of DNA coding for the desired gene product (*ie* "exogenous DNA") by using, most typically, a drug resistant gene, referred to as a "dominant selectable marker," that allows for selection of cells that have integrated the exogenous DNA. Stated again, those cells which properly incorporate the exogenous DNA including, *eg*, the drug resistant gene, will
20 maintain resistance to the corresponding drug. This is most typically followed by co-amplification of the DNA encoding for the desired gene product in the transfected cell by amplifying an adjacent gene that also encodes for drug resistance ("amplification gene"), *eg* resistance to methotrexate (MTX) in the case of dehydrofolate reductase (DHFR) gene. The amplification gene can be the
25 same as the dominant selectable marker gene, or it can be a separate gene. (As those in the art appreciate, "transfection" is typically utilized to describe the process or state of introduction of a plasmid into a mammalian host cell, while "transformation" is typically utilized to describe the process or state of introduction of a plasmid into a bacterial host cell).

Two amplification approaches are typically employed by those in the art. In the first, the entire population of transfected and drug resistant cells (each cell comprising at least one integration of the gene encoding for drug resistance) is amplified; in the second, individual clones derived from a single cell are amplified. Each approach has unique advantages.

With respect to the first approach, it is somewhat "easier" to amplify the entire population (typically referred to as a "shotgun" approach, an apt description) compared to individual clones. This is because amplification of individual clones initially involves, *inter alia*, screening of hundreds of isolated mammalian colonies (each derived from a single cell, most of which being single copy integrants of the expression plasmid) in an effort to isolate the one or two "grail" colonies which secrete the desired gene product at a "high" level, *ie* at a level which is (typically) three orders of magnitude higher than the lowest detectable expression level. These cells are also often found to have only a single copy integration of the expression plasmid. Additionally, amplifying individual clones results in production cell lines which contain fewer copies of the amplified gene as compared to amplification of all transfected cells (typically, 10-20 versus 500-1000).

With respect to the second approach, production cell lines derived from amplifying individual clones are typically derived in lower levels of the drug(s) used to select for those colonies which comprise the gene for drug(s) resistance and the exogenous gene product (*ie* in the case of methotrexate and DHFR, 5nM versus 1 μ M). Furthermore, individual clones can typically be isolated in a shorter period of time (3-6 months versus 6-9 months).

Ideally then, the tangible benefits of both approaches should be merged: at a practical level, this would involve decreasing the number of colonies to be screened, and increasing the amount product secreted by these colonies. The present invention accomplishes this task.

5

The position where the DNA of the dominant selectable marker of the plasmid DNA is integrated within the cellular DNA of the host cell determines the level of expression of the dominant selectable marker protein, as is recognized by those in the art. It is assumed that the expression of a gene encoding a protein of interest which is either co-linked to or positioned near the dominant selectable marker DNA is proportional to the expression of the dominant selectable marker protein. While not wishing to be bound by any particular theory, the inventor has postulated that if the gene used to select for the integration of the exogenous DNA in the mammalian cell (*ie* the dominant selectable marker) was designed such that translation of that dominant selectable marker was impaired, then only those plasmids which could overcome such impairment by over-production of the gene product of the dominant selectable marker would survive, *eg*, the drug-screening process. By associating the exogenous DNA with the dominant selectable marker, then, *a fortiori*, over-production of the gene product of the dominant selectable marker would also result in over-production of the gene product derived from the associated exogenous DNA. In accordance with this postulated approach, impairment of translation of the dominant selectable marker gene would be necessary, and an avenue for such impairment was the consensus Kozak portion of the gene.

25

By comparing several hundred vertebrate mRNAs, Marilyn Kozak in "Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes," *Nuc. Acids Res.* 9: 5233-5252 (1981) and "Compilation and analysis of sequences upstream from the translational start site in eukaryotic

mRNAs," *Nuc. Acids Res.* 12: 857-872 (1984), proposed the following "consensus" sequence for initiation of translation in higher eukaryotes:

5 -3 +1
 cc Acc AUG G

(As those in the art appreciate, uracil, U, replaces the deoxynucleotide thymine, T, in RNA.) In this sequence, referred to as a "consensus Kozak," the most highly conserved nucleotides are the purines, A and G, shown in capital letters above; mutational analysis confirmed that these two positions have the strongest influence on initiation. See, eg, Kozak, M. "Effects of intercistronic length on the efficiency of reinitiation of eukaryotic ribosomes." *Mol. Cell Bio.* 7/10: 3438-3445 (1987). Kozak further determined that alterations in the sequence upstream of the consensus Kozak can effect translation. For example, in "Influences of mRNA secondary structure on initiation by eukaryotic ribosomes." *PNAS* 83: 2850-2854 (1986) Kozak describes the "artificial" introduction of a secondary hairpin structure region upstream from the consensus Kozak in several plasmids that encoded preproinsulin; it was experimentally determined that a stable stem loop structure inhibited translation of the preproinsulin gene, reducing the yield of proinsulin by 85-95%.

Surprisingly, it was discovered by the inventor that by changing the purines A(-3 vis-a-vis ATG start codon) and G(+1) to pyrimidines, translation impairment was significant: when the consensus Kozak for the neomycin phosphotransferase gene was subjected to such alterations (as will be set forth in detail below), the number of G418 resistant colonies significantly decreased; however, there was a significant increase in the amount of gene product expressed by the individual G418 resistant clones. As those in the art will recognize, this has the effect of increasing the efficiency of the expression system—there are less colonies to screen, and most of the colonies that are viable produce significantly more

product than would ordinarily be obtained. Confirmation of the inventor's postulated theory was thus experimentally determined.

- 5 As noted, for purposes of this patent document a, "consensus Kozak" comprises the following sequence:

$$\begin{array}{ccc} -3 & & +1 \\ \text{Pxx} & \text{ATG} & \text{Pxx} \end{array}$$

- 10 a "partially impaired consensus Kozak" comprises the following sequence

$$\begin{array}{ccc} -3 & & +1 \\ \text{P/Pyxx} & \text{ATG} & \text{P/Pyxx} \end{array}$$

- 15 and a disclosed and claimed "fully impaired consensus Kozak" comprises the following sequence:

$$\begin{array}{ccc} -3 & & +1 \\ \text{Pyxx} & \text{ATG} & \text{Pyxx} \end{array}$$

20

- where: "x" is a nucleotide selected from the group consisting of adenine (A), guanine (G), cytosine (C) or thymine (T) (uracil, U, in the case of RNA); "P" is a purine, *ie* A or G, "Py" is a pyridine, *ie* C or T/U; ATG is a conventional start codon which encodes for the amino acid methionine (Met); the numerical
- 25 designations are relative to the ATG codon, *ie* a negative number indicates "upstream" of ATG and a positive number indicates "downstream" of ATG; and for the partially impaired consensus Kozak, the following proviso is applicable-- only one of the -3 or +1 nucleotides is a pyridine, *eg*, if -3 is a pyridine, then +1 must be a purine or if -3 is a purine, then +1 must be a pyridine. Most
- 30 preferably, the fully impaired consensus Kozak is associated with the site of translation initiation of a dominant selectable marker which is preferably (but not necessarily) co-linked to exogenous DNA which encodes for a gene product of interest. As used herein, "nucleotide" is meant to encompass natural and

synthetic deoxy- and ribonucleotides as well as modified deoxy- and ribonucleotides, *ie* where the 3' OH, 5'OH, sugar and/or heterocyclic base are modified, as well as modification of the phosphate backbone, *eg* methyl phosphates, phosphorothioates and phosphoramidites.

5

Information regarding the gene sequence of the dominant selectable marker is preferably known; however, in lieu of the entire sequence, information regarding the nucleic acid sequence (or amino acid sequence) at the site of translation initiation of the dominant selectable marker must be known. Stated again, in order to effectuate a change in the consensus or partially impaired consensus Kozak, one must know the sequence thereof. Changing the consensus or partially impaired consensus Kozak to a fully impaired consensus Kozak sequence can be accomplished by a variety of approaches well known to those in the art including, but not limited to, site specific mutagenesis and mutation by primer-based amplification (*eg* PCR); most preferably, such change is accomplished via mutation by primer-based amplification. This preference is principally based upon the comparative "ease" in accomplishing the task, coupled with the efficacy associated therewith. For ease of presentation, a description of the most preferred means for accomplishing the change to a fully impaired consensus Kozak will be provided.

10
15
20

In essence, mutation by primer-based amplification relies upon the power of the amplification process itself--as PCR is routinely utilized, focus will be directed thereto. However, other primer-based amplification techniques (*eg* ligase chain reaction, etc.) are applicable. One of the two PCR primers ("mutational primer") incorporates a sequence which will ensure that the resulting amplified DNA product will incorporate the fully impaired consensus Kozak within the transcriptional cassette incorporating the dominant selectable marker of interest; the other PCR primer is complementary to another region of the

25

dominant selectable marker; a transcriptional cassette incorporating the dominant selectable marker; or a vector which comprises the transcriptional cassette. By way of example, the complement to a dominant selectable marker which includes a consensus Kozak could have the following sequence (SEQ ID

5 NO: 1):

3'-tagctaggTccTACCcc-5'

10 In order to create a fully impaired consensus Kozak, the mutational primer could have the following sequence (SEQ ID NO: 2) (for convenience, SEQ ID NO: 1 is placed over the mutational primer for comparative purposes):

5'-atcgatccTggATGCgg-3'
3'-tagctaggTccTACCcc-5'

15

As is evident, complementarity is lacking in the primer (see, the "*" symbols). By utilizing excess mutational primer in the PCR reaction, when the sequence including the consensus Kozak is amplified, the resulting amplified DNA products will incorporate the mutations such that as the amplified DNA products are in turn amplified, the mutations will predominate such that a fully impaired consensus Kozak will be incorporated into the amplification product.

25 Two criteria are required for the mutational primer--first, the length thereof must be sufficient such that hybridization to the target will result. As will be appreciated, the mutational primer will not be 100% complementary to the target. Thus, a sufficient number of complementary bases are required in order to ensure the requisite hybridization. Preferably, the length of the mutational primer is between about 15 and about 60 nucleotides, more preferably between about 18 and about 40 nucleotides, although longer and shorter lengths are viable. (To the extent that the mutational primer is also utilized to incorporate

an out-of-frame start codon or secondary structure, the length of the mutational primer can correspondingly increase). Second, the ratio of mutational primer to target must be sufficiently excessive to "force" the mutation. Preferably, the ratio of mutational primer to target is between about 250:1 to about 5000:1, more preferably between about 400:1 to about 2500:1, and most preferably between about 500:1 to about 1000:1.

Because the parameters of a PCR reaction are considered to be well within the level of skill of those in the art, details regarding the particulars of that reaction are not set forth herein; the skilled artisan is readily credited with recognizing the manner in which this type of mutation can be accomplished using PCR techniques - the foregoing is provided as a means of providing elucidation as opposed to detailed edification.

As noted, it is most preferred that the fully impaired consensus Kozak is associated with the site of translation initiation of a dominant selectable marker incorporated into a transcriptional cassette which forms a part of an expression vector. Preferred dominant selectable markers include, but are not limited to: herpes simplex virus thymidine kinase; adenosine deaminase; asparagine synthetase; *Salmonella* his D gene; xanthine guanine phosphoribosyl transferase ("XGPRT"); hygromycin B phosphotransferase; and neomycin phosphotransferase ("NEO"). Most preferably, the dominant selectable marker is NEO.

The dominant selectable marker herpes simplex virus thymidine kinase is reported as having the following partially impaired consensus Kozak:

 -3 +1
cg Cgt ATG Gct

30

See, Heller, S. "Insertional Activities of a Promotorless Thymidine Kinase Gene," *Mol. & Cell. Bio.* 8/8:3218-3302, Figure 4, nucleotide 764. By changing the +1 purine (G) to a pyrimidine (C or T/U), a fully impaired Kozak as defined herein is generated (the -3 of the herpes simplex virus thymidine kinase is a pyrimidine).

5 Changing +1 purine to a pyrimidine also has the effect of changing the encoded amino acid from alanine (GCT) to proline (CCT) or serine (TCT); it is preferred that conservative amino acid changes result from the changes to the nucleotides. Thus, it is preferred that the change to TCT be made because the change from alanine to serine is a more conservative amino acid change than changing

10 alanine to proline.

Histidinol dehydrogenase is another dominant selectable marker. See, Hartmen, S.C. and Mulligan, R.C. "Two dominant acting selectable markers for gene transfer studies in mammalian cells," *PNAS* 85:8047-8051 (1988). The *his D*

15 gene of *Salmonella typhimurium* has the following partially impaired consensus Kozak:

-3 +1
gc Aga ATG Tta

20

As -3 is a purine, changing -3 to a pyrimidine (C or T/U) results in a fully impaired consensus Kozak; as is appreciated, because these nucleotides are upstream of the start codon, no impact on amino acid translation results from this change.

25

Hygromycin B phosphotransferase is another dominant selectable marker; the reported sequence for the *hph* gene (see, Gritz, L. and Davies, J. "Plasmid encoded hygromycin B resistance: the sequence of hygromycin B phosphotransferase gene and its expressing in *Escherichia coli* and

Saccharomyces cerevisiae" Gene 25:179-188, 1983) indicates that the consensus Kozak is:

-3 +1
ga Gat ATG Aaa

5 Both -3 and +1 are purines; thus changing -3 and +1 to pyrimidines results in a fully impaired consensus Kozak (this results in the following encoded amino acids: +1 to C - glutamine; +1 to T - stop codon. Because this codon is downstream of the start codon, the change to the stop codon TAA should not be
10 accomplished).

XGPRT is another dominant selectable marker. The reported partially impaired consensus Kozak of XGPRT has the following sequence:

15 -3 +1
 tt Cac ATG Agc

See, Mulligan, R.C. and Berg, P. "Factors governing the expression of a bacterial gene in mammalian cells." *Mol. & Cell Bio.* 1/5:449-459 (1981), Figure 6. By
20 changing the +1 purine to a pyrimidine, a fully impaired consensus Kozak is created; the effect on the encoded amino acid (AGC-serine) is as follows: CGC-arginine; TGC-cysteine.

Adenosine deaminase (ADA) can also be utilized as a dominant selectable
25 marker. The reported consensus Kozak sequence for adenosine deaminase is:

-3 +1
ga Acc ATG Gcc

30 See, Yeung, C.Y. *et al.*, "Identification of functional murine adenosine deaminase cDNA clones by complementation in *E. coli*," *J. Bio. Chem.* 260/18:10299-10307 (1985), Figure 3. By changing both -3 and +1 purines to pyrimidines, fully impaired consensus Kozak sequences result. The encoded amino

acid corresponding to GCC (alanine) is changed to either proline (CCC) or serine (TCC), with the change to serine being preferred, due to the conservative nature of this change.

- 5 The reported partially impaired consensus Kozak for asparagine synthetase is as follows:

10 -3 +1
 gc Acc ATG Tgt

See, Andrulis, I.L. *et al.*, "Isolation of human cDNAs for asparagine synthetase and expression in Jensen rat sarcoma cells," *Mol. Cell. Bio.* 7/7:2435-2443 (1987). Changing the +3 purine to a pyrimidine results in a fully impaired consensus Kozak.

15

The partially impaired consensus Kozak for neomycin phosphotransferase (which includes an upstream out of frame start codon) is as follows:

20 -3 +1
 gga TGg gga tcg ttt Cgc ATG Att

Changing the +1 purine to a pyrimidine has the effect of creating a fully impaired consensus Kozak (changes to the encoded amino acid isoleucine, ATT are as follows: CTT - leucine and TTT-phenylalanine, with the change to leucine
25 being preferred, due to the conservative nature of this change).

The foregoing is not intended, nor is it to be construed as limiting; rather, in the context of the disclosed invention, the foregoing is presented in an effort to provide equivalent examples of changes in the reported consensus Kozak
30 sequences or partially impaired consensus Kozak sequences of several well-known dominant selectable markers.

As noted, a most preferred dominant selectable marker is NEO. Particularly preferred fully impaired consensus sequences for NEO are as follows:

5

Txx ATG Ctt (SEQ ID NO: 3)
Cxx ATG Ctt (SEQ ID NO: 4)
Txx ATG Ttt (SEQ ID NO: 5)
Cxx ATG Ttt (SEQ ID NO: 6)

10

where x are nucleotides. SEQ. ID. NO. 3 is most preferred; and xx are preferably CC.

Other transcriptional cassettes, which may or may not include a fully impaired
15 consensus Kozak, can be incorporated into a vector which includes
transcriptional cassettes containing the disclosed and claimed fully impaired
consensus Kozak; such "other transcriptional cassettes" typically are utilized to
allow for "enhancement," "amplification" or "regulation" of gene product
repression. For example, co-transfection of the exogenous DNA with the
20 dehydrofolate reductase (DHFR) gene is exemplary. By increasing the levels the
antifolate drug methotrexate (MTX), a competitive inhibitor of DHFR, presented
to such cells, an increase in DHFR production can occur via amplification of the
DHFR gene. Beneficially, extensive amounts of flanking exogenous DNA will
also become amplified; therefore, exogenous DNA inserted co-linear with an
25 expressible DHFR gene will also become overexpressed. Additionally,
transcriptional cassettes which allow for regulation of expression are available.
For example, temperature sensitive COS cells, derived by placing SV40ts mutant
large T antigen gene under the direction of Rous sarcoma virus LTR (insensitive
to feedback repression by T antigen), has been described. *See, 227 Science* 23-28
30 (1985). These cells support replication from SV40 *ori* at 33°C but not at 40°C
and allow regulation of the copy number of transfected SV40 *ori*-containing
vectors. The foregoing is not intended, nor is it to be construed, as limiting;

rather the foregoing is intended to be exemplary of the types of cassettes which can be incorporated into expression vectors comprising the disclosed fully impaired consensus Kozak. The skilled artisan is credited with the ability to determine the specific type of other transcriptional cassettes, *vis-a-vis* the objective of the expression system, which are applicable and which can be advantageously exploited.

As indicated above, in particularly preferred embodiments of the invention, at least one out-of-frame start codon (*ie* ATG) is located upstream of the fully impaired consensus Kozak start codon, without a stop codon being located between the out-of-frame start codon and the fully impaired consensus Kozak start codon. The intent of the out-of-frame start codon is to, in effect, further impair translation of the dominant selectable marker.

As used herein, the term "stop codon" is meant to indicate a "nonsense codon," *ie* a codon which does not encode one of the 20 naturally occurring amino acids such that translation of the encoded material terminates at the region of the stop codon. This definition includes, in particular, the traditional stop codons TAA, TAG and TGA.

As used herein, the term "out-of-frame" is relative to the fully impaired consensus Kozak start codon. As those in the art appreciate, in any DNA macromolecule (or RNA macromolecule) for every in-frame sequence, there are two out-of-frame sequences. Thus, for example, with respect to the following sequence incorporating a fully impaired consensus Kozak:

$$\begin{array}{ccccccc} & & & -3 & & +1 & \\ \text{gcA} & \text{TGc} & \text{cAT} & \text{Ggc} & \text{Cxx} & \text{ATG} & \text{Cxx} \end{array}$$

the in-frame codons are separated by triplets, *eg*, gcA, TGc, cAT and Ggc; the out-of-frame codons would include, *eg* cAT, ATG, Gcc, ccA, ATG and TGg. Thus, two

start codons (in capital letters and underlined>) are out-of-frame relative to the start codon of the fully impaired consensus Kozak.

- When such an out-of-frame start codon is utilized, it is preferred that this be within about 1000 nucleotides upstream of the fully impaired consensus Kozak start codon, more preferably within about 350 nucleotides upstream of the fully impaired consensus Kozak start codon, and most preferably within about 50 nucleotides of the fully impaired consensus Kozak start codon.
- As is appreciated, the upstream sequence can be manipulated to achieve positioning at least one out-of-frame sequence upstream of the fully impaired consensus Kozak start codon using (most preferably) a mutational primer used in the type of amplification protocol described above.
- Utilization of a fully impaired consensus Kozak start codon located within a secondary structure (ie a "stem-loop" or "hairpin") is beneficially viable to impairment of translation of the protein encoded by the dominant selectable marker. In such an embodiment, it is preferred that this start codon be located within the stem of a stem loop secondary structure. These, by way of schematic example, in such an embodiment, the start codon of the fully impaired consensus Kozak is positioned as follows:

```

      T
      x   x
      x x
      x A
      x T
      x G
x A TGxx Cxx

```

(An out-of-frame start codon which is not part of the secondary structure is also represented.) As is appreciated, within the stem loop, complementarity along the stem is, by definition, typically required. For exemplary methodologies

regarding, *inter alia*, introduction of such secondary structures into the sequence, as well as information regarding secondary structure stability, see, Kozak, *PNAS*, 1986, *supra*.

5 As noted, it is preferred that a dominant selectable marker with a naturally occurring intronic insertion region or an artificially created intronic insertion region be utilized and at least one gene product of interest inserted within this region. While not wishing to be bound by any particular theory, the inventor postulates that such an arrangement increases expression efficiency because the
10 number of viable colonies that survive the selection process *via-a-vis* the dominant selectable marker will decrease; the colonies that do survive the selection process will, by definition, have expressed the protein necessary for survival, and in conjunction therewith, the gene product of interest will have a greater tendency to be expressed. As further postulated, the RNA being
15 transcribed from the gene product of interest within the intronic insertion region interferes with completion of transcription (elongation of RNA) of the dominant selectable marker; therefore, the position that the dominant selectable marker is integrated within the cellular DNA is likely to be a position where a larger amount of RNA is initially transcribed.

20

As is appreciated, prokaryotic proteins do not typically include splices and introns. However, the majority of dominant selectable markers which are preferred for expression vector technology are derived from prokaryotic systems. Thus, when prokaryotic-derived dominant selectable markers are utilized, as is
25 preferred, it is often necessary to generate an artificial splice within the gene so to create a location for insertion of an intron comprising the gene product of interest. It is noted that while the following rules are provided for selection of a splice site in prokaryotic genes, they can be readily applied to eukaryotic genes.

A general mechanism for the splicing of messenger RNA precursors in eukaryotic cells is delineated and summarized in Sharp, Philip A. "Splicing of Messenger RNA Precursors" *Science*, 235: 736-771 (1987) (see, in particular, Figure 1) which is incorporated herein by reference. Based upon Sharp, there are four minimum criteria in the nucleic acid sequence which are necessary for a splice: (a) 5' splice donor; (b) 3' splice acceptor; (c) branch point, and (d) polypyrimidine tract. The consensus sequences for the 5' splice donor is reported to be

C A
AAG/GTGAGT and for the 3' splice acceptor, NCAG/G (where a "/" symbol indicates the splice site); see, Mount, S.M. "A Catalogue of Splice Junction Sequences" *Nuc. Acids. Res.* 10/2:459-472 (1992) which is incorporated herein by reference. The consensus sequence for the branch point, i.e. the location of the lariat formation with the 5' splice donor, is reported as PyNPyPAPy; and the reported preferred branch site for mammalian RNA splicing is TACTAAC (Zhuang, Y. et al. "UACUAAC is the preferred branch site for mammalian mRNA splicing" *PNAS* 86: 2752-2756 (1989), incorporated herein by reference). Typically, the branch point is located at least approximately 70 to about 80 base-pairs from the 5'-splice donor (there is no defined upper limit to this distance). The poly pyrimidine tract typically is from about 15 to about 30 base pairs and is most typically bounded by the branch point and the 3' splice acceptor.

The foregoing is descriptive of the criteria imposed by nature on naturally occurring splicing mechanisms. Because there is no exact upper limit on the number of base pairs between the 5' splice donor and the branch point, it is preferred that the gene product of interest be inserted within this region in situations where a natural intron exists within the dominant selectable marker. However, as noted, such introns do not exist within most of the preferred dominant selectable markers; as such, utilization of artificial introns are preferably utilized with these markers.

In order to generate an artificial intron, a "splice donor:splice acceptor" site must be located within the encoding region of the dominant selectable marker. Based upon Sharp and Mount, it is most preferred that the following sequence function as the splice donor:splice acceptor site -- CAGG (with the artificial splice occurring at the GG region). A preferred sequence is AAGG.

Focusing in on the most preferred sequence CAGG, the following codons and amino acids can be located within the encoding region of the dominant selectable marker for generation of the artificial intronic insertion region:

A		B		C	
<u>CAG/</u>	<u>GNN</u>	<u>NCA</u>	<u>G/GN</u>	<u>NNC</u>	<u>AG/G</u>
Gln	Ala	Ala	Gly	Ala	Leu
	Asp	Pro		Arg	Phe
	Gly	Ser		Asn	Pro
	Glu	Thr		Asp	Ser
	Val			Cys	Thr
				Gly	Tyr
				His	Val
					Ile

(As will be appreciated, the same approach to determining viable amino acid residues can be utilized for the preferred sequence of AAGG). The most preferred codon group for derivation of the splice donor:splice acceptor site is group A. Once these amino acid sequences are located, a viable point for generation of an artificial intronic insertion region can be defined.

Focusing on the preferred NEO dominant selectable marker, amino acid residues Gln Asp (codon group A) are located at the positions 51 and 52 of NEO and amino acid residues Ala Arg (codon group C) are located at positions 172 and 173 (as is appreciated, multiple artificial intronic insertion regions may be utilized). Focusing on residues 50 - 53 of NEO, the nucleic acid and amino acid sequences are as follows:

50 51 52 53
 5' CTG CAG GAC GAG 3'
 Leu Gln Asp Glu

Accordingly, an artificial intronic insertion region can be generated between
 0 residues 51 and 52 of NEO. This region most preferably comprises a branch
 point, a polypyrimidine tract and, preferably, a region for insertion of a gene
 product of interest, ie a region amenable to enzymatic digestion.

Two criteria are import for the artificial intronic insertion region: the first two
 10 nucleic acid residues of the 5' splice site (eg abutting CAG) are most preferably
 GT and the first two nucleic acid residues of the 3' splice site (eg abutting G) are
 most preferably AG.

Using the criteria defined above, an artificial intronic insertion region was
 15 between amino acid residues 51 and 52 of NEO:

50 NEO 51 52 NEO 53
 LEU GLN Branch Polypyrimide Tract ASP GLU 3'
 5' CTG CAGGTAAGT GCGGCCGC TACTAAC(TC)₃ CTC(T)₃ TCC(T)₅ C CTGCAG/GAC GAG
 Not I

20 (Details regarding the methology for creating this artificial intronic insertion
 region are set forth in the Example Section to follow). The Not I site was created
 as the region where the gene product of interest can be incorporated. Therefore,
 upon incorporation, the gene product of interest is located between amino acid
 25 residues 51 and 52 of NEO, such that during NEO transmission, the gene
 product of interest will be "spliced-out".

The host cell line is most preferably of mammalian origin; those skilled in the art
 are credited with ability to preferentially determine particular host cell lines
 30 which are best suited for the desired gene product to be expressed therein.
 Exemplary host cell lines include, but are not limited to, DG44 and DXBII

carcinoma), CV1 (monkey kidney line), COS (a derivative of CV1 with SV40 T antigen), R1610 (Chinese hamster fibroblast) BALBC/3T3 (mouse fibroblast), HAK (hamster kidney line), SP2/O (mouse myeloma), P3x63-Ag3.653 (mouse myeloma), BFA-lclBPT (bovine endothelial cells), RAJI (human lymphocyte) and
5 293 (human kidney). Host cell lines are typically available from commercial services, the American Tissue Culture Collection or from published literature.

Preferably the host cell line is either DG44 or SP2/O. See, Urland, G. *et al.*, "Effect of gamma rays and the dihydrofolate reductase locus: deletions and
10 inversions." *Som. Cell & Mol. Gen.* 12/6:555-566 (1986) and Shulman, M. *et al.*, "A better cell line for making hybridomas secreting specific antibodies." *Nature* 276:269 (1978), respectively. Most preferably, the host cell line is DG44. Transfection of the plasmid into the host cell can be accomplished by any technique available to those in the art. These include, but are not limited to,
15 transfection (including electrophoresis and electroporation), cell fusion with enveloped DNA, microinjection, and infection with intact virus. See, Ridgway, A.A.G. "Mammalian Expression Vectors." Chapter 24.2, pp. 470-472 *Vectors*, Rodriguez and Denhardt, Eds. (Butterworths, Boston, MA 1988). Most preferably, plasmid introduction into the host is via electroporation.

20

EXAMPLES

The following examples are not intended, nor are they to be construed, as limiting the invention; the examples are intended to demonstrate the
25 applicability of an embodiment of the invention disclosure herein. The disclosed fully impaired consensus Kozak sequence is intended to be broadly applied as delineated above. However, for presentational efficiency, exemplary uses of particularly preferred embodiments of fully impaired consensus Kozak sequences

are utilized in conjunction with tandem chimeric antibody expression vectors (also referred to herein as antibody expression vectors) as disclosed below.

I. TANDEM CHIMERIC ANTIBODY EXPRESSION ("TCAE") VECTOR

5

B cell lymphocytes arise from pluripotent stem cells and proceed through ontogeny to fully matured antibody secreting plasma cells. The human B lymphocyte-restricted differentiation antigen Bp35, referred to in the art as "CD20," is a cell surface non-glycosylated phosphoprotein of 35,000 Daltons; 10 CD20 is expressed during early pre-B cell development just prior to the expression of cytoplasmic μ heavy chains. CD20 is expressed consistently until the plasma cell differentiation stage. The CD20 molecule regulates a step in the activation process which is required for cell cycle initiation and differentiation. Because CD20 is expressed on neoplastic B cells, CD20 provides a promising 15 target for therapy of B cell lymphomas and leukemias. The CD20 antigen is especially suitable as a target for anti-CD20 antibody mediated therapy because of accessibility and sensitivity of hematopoietic tumors to lysis via immune effector mechanisms. Anti-CD20 antibody mediated therapy, *inter alia*, is disclosed in co-pending Serial No. 07/978,891 and Serial No. _____, filed 20 simultaneously herewith. The antibodies utilized are mouse/human chimeric anti-CD20 antibodies expressed at high levels in mammalian cells (chimeric anti-CD20"). This antibody was derived using vectors disclosed herein, to wit: TCAE 5.2; ANEX 1; ANEX 2; GKNEOSPLA3F; and NEOSPLA3F (an additional vector, TCAE 8, was also utilized to derive chimeric anti-CD20 antibody -- TCAE 25 8 is identical to TCAE 5.2 except that the NEO translational start site is a partially impaired consensus Kozak. TCAE 8 is described in the co-pending patent document filed herewith.).

In commonly-assigned United States Serial Number 07/912,292, disclosed, *inter alia*, are human/Old World monkey chimeric antibodies; an embodiment of the invention disclosed therein are human/monkey chimeric anti-CD4 antibodies in vector TCAE 6 (see, Figure 6 of Serial Number 07/912,292, and corresponding discussion). TCAE 6 is substantially identical to TCAE 5.2; TCAE 6 contains human lambda constant region, while TCAE 5.2 contains human kappa constant region. TCAE 5.2 and ANEX 1 (referred to in that patent document as TCAE 12) are disclosed as vectors which can be utilized in conjunction with human/Old World monkey chimeric antibodies. The comparative data set forth in Serial No. 07/912,292 vis-a-vis TCAE 5.2 and ANEX 1 is relative to expression of chimeric anti-CD20 antibody.

TCAE 5.2 was derived from the vector CLDN, a derivative of the vector RLDN10b (see, 253 *Science* 77-91, 1991). RLDN10b is a derivative of the vector TND (see, 7*DNA* 651-661, 1988). The vector "family line" is as follows: TDN → RLDN10b → CLDN → TCAE 5.2 → ANEX 1 (the use of the "→" symbol is not intended, nor is it to be construed, as an indication of the effort necessary to achieve the changes from one vector to the next; e.g. to the contrary, the number and complexity of the steps necessary to generate TCAE 5.2 from CLDN were extensive).

TND was designed for high level expressions of human tissue plasminogen activator. RLDN10b differs from TND in the following ways: the dihydrofolate reductase ("DHFR") transcriptional cassette (comprising promoter, murine DHFR cDNA, and polyadenylation region) was placed in between the tissue plasminogen activator cassette ("t-PA expression cassette") and the neomycin phosphotransferase ("NEO" cassette") so that all three cassettes were in tandem and in the same transcriptional orientation. The TND vector permitted selection with G418 for cells carrying the DHFR, NEO and t-PA genes prior to selection

for DHFR gene amplification in response to methotrexate, MTX. The promoter in front of the DHFR gene was changed to the mouse beta globin major promoter (see, 3 *Mol. Cell Bio.* 1246-1254, 1983). Finally, the t-PA cDNA was replaced by a polylinker such that different genes of interest can be inserted in the polylinker.

- 5 All three eukaryotic transcriptional cassettes (t-PA, DHFR, NEO) of the TND vector can be separated from the bacterial plasmid DNA (pUC19 derivative) by digestion with the restriction endonuclease Not I.

- 10 CLDN differs from RLDN10b in the following ways: The Rous LTR, positioned in front of the polylinker, was replaced by the human cytomegalovirus immediate early gene promoter enhancer ("CMV"), (see, 41 *Cell* 521, 1985), from the Spe I site at -581 to the Sst I site at -16 (these numbers are from the *Cell* reference).

- 15 As the name indicates, TCAE vectors were designed for high level expressions of chimeric antibody. TCAE 5.2 differs from CLDN in the following ways:

- A. TCAE 5.2 comprises four (4) transcriptional cassettes, as opposed to three (3), and these are in tandem order, *ie* a human immunoglobulin light chain absent a variable region; a human immunoglobulin heavy chain absent a variable region; DHFR; and NEO. Each transcriptional cassette contains its own eukaryotic promoter and polyadenylation region (reference is made to Figure 2 which is a diagrammatic representation of the TCAE 5.2 vector). The CMV promoter/enhancer in front of the immunoglobulin heavy chain is a truncated version of the promoter/enhancer in front of the light chain, from the Nhe I site at -350 to the Sst I site at -16 (the numbers are from the *Cell* reference, *supra*).
25 Specifically,

- 1) A human immunoglobulin light chain constant region was derived via amplification of cDNA by a PCR reaction. In TCAE 5.2, this was the human

- immunoglobulin light chain kappa constant region (Kabat numbering, amino acids 108-214, allotype Km 3), and the human immunoglobulin heavy chain gamma 1 constant region (Kabat numbering amino acids 114-478, allotype Gmla, Gmlz). The light chain was isolated from normal human blood (IDEC Pharmaceuticals Corporation, La Jolla, CA); RNA therefrom was used to synthesize cDNA which was then amplified using PCR techniques (primers were derived vis-a-vis the consensus Kabat). The heavy chain was isolated (using PCR techniques) from cDNA prepared from RNA which was in turn derived from cells transfected with a human IgG1 vector (*see*, 3 *Prot. Eng.* 531, 1990; vector pN_γ162). Two amino acids were changed in the isolated human IgG1 to match the consensus amino acid sequence in Kabat, to wit: amino acid 225 was changed from valine to alanine (GTT to GCA), and amino acid 287 was changed from methionine to lysine (ATG to AAG);
- 15 2) The human immunoglobulin light and heavy chain cassettes contain synthetic signal sequences for secretion of the immunoglobulin chains;
- 3) The human immunoglobulin light and heavy chain cassettes contain specific DNA restriction sites which allow for insertion of light and heavy
20 immunoglobulin variable regions which maintain the transitional reading frame and do not alter the amino acids normally found in immunoglobulin chains;
- 4) The DHFR cassette contained its own eukaryotic promoter (mouse beta globin major promoter, "BETA") and polyadenylation region (bovine growth
25 hormone polyadenylation, "BGH"); and
- 5) The NEO cassette contained its own eukaryotic promoter (BETA) and polyadenylation region (SV40 early polyadenylation, "SV").

5

10

20

30

product (less than 25 ng/ml), while 62 of these colonies were expressing greater than 100 ng/ml; of these 62 colonies, nearly 23 were expressing over 250 ng/ml (23%), with 6 expressing greater than 1000 ng/ml (6%).

5 The foregoing evidences, *inter alia*, the following: 1) because the difference between TCAE 5.2 and ANEX 1 was limited to the Kozak translation start site of the NEO gene, and because the gene product of interest (chimeric anti-CD20 antibody) was co-linked to the NEO gene, a conclusion to be drawn is that these differences in results are attributed solely to the differences in the Kozak
10 translation start site; 2) it was experimentally confirmed that utilization of a fully impaired consensus Kozak in conjunction with a dominant selectable marker resulted in significantly less viable colonies; 3) it was experimentally confirmed that utilization of a fully impaired consensus Kozak in conjunction with a dominant selectable marker co-linked to a desired gene product
15 significantly increased the amount of expressed gene product. Thus, the number of colonies to be screened decreased while the amount of expressed gene product increased.

20 II. IMPACT OF OUT-OF-FRAME START SEQUENCE

Conceptually, further impairment of translation initiation of the dominant selectable marker of ANEX 1 could be effectuated by utilization of at least one out-of-frame ATG start codon upstream of the neomycin phosphotransferase start codon. Taking this approach one step further, utilization of a secondary
25 structure ("hairpin") which incorporated the *neo* start codon within the stem thereof, would be presumed to further inhibit translation initiation. Thus, when the out-of-frame start codon/fully impaired consensus Kozak was considered, this region was designed such that the possibility of such secondary structures was increased.

As indicated previously, the Kozak region for the *neo* start codon in the ANEX 1 vector is:

TTGGGAGCCTTGG ATCGAT CC Tcc ATG Ctt

5

The desired sequence for a vector identical to ANEX 1 but incorporating the above-identified changes vis-a-vis the *neo* start codon, referred to as ANEX 2, is as follows (SEQ ID NO: 9):

10 CCA GCA TGG AGG A ATCGAT CC Tcc ATG Ctt

(The out-of-frame start codon is underlined.) The fully impaired consensus Kozak of ANEX 2 is identical to that of ANEX 1. The principal difference is the inclusion of the upstream out-of-frame start codon. A possible difference is the
15 formation of a secondary structure involving this sequence, proposed as follows:

```

      CG   }
      T A  }  CLA I site
      A T  }
20      AT
      GC
      GC
      AT
      GC
25      GC
      TA
      AT
      CG
      GC
30      AT
      CT
      CG

```

The sequence in bold, ATG, is the upstream out-of-frame start codon; the "loop"
35 portion of the secondary structure is the CLA I site; and the sequence between the "T" and "C" (italics and bold) is the start codon (underlined) of the fully impaired consensus Kozak.

In order to effectuate this change, a PCR fragment was cloned into anti-CD20 in ANEX 1 from Xho I (5520) to Cla I (5901); see, Figure 4. Primers were as follows:

5 3'-Primer 489 (SEQ ID NO: 10):

10 5'-GGA GGA TCG ATT CCT CCA TGC TGG
CAC AAC TAT GTC AGA AGC AAA TGT
GAG C-3'

The upper-lined portion of Primer 489 is a Cla I site; the under-lined portion is the fully impaired consensus Kozak translation start site.

15 5'-Primer 488 (SEQ. ID. NO. 11):

5'-CTG GGG CTC GAG CTT TGC-3'

The upper-lined portion of Primer 485 is an Xho I site.

20

These primers were prepared using an ABI 391 PCR MATE™ DNA synthesizer (Applied Biosystems, Foster City, CA). Phosphoramidites were obtained from Cruachem (Glasgow, Scotland): dA(bz) - Prod. No. 20-8120-21; dG(ibu) - Prod. No. 20-8110-21; dC(bz) - Prod. No. 20-8130-21; T - Prod. No. 20-8100-21.

25

Conditions for the PCR reaction using these primers were as follows: 2λ ("microliters") of anti-CD20 in TCAE 5.2 in plasmid grown in *E. coli* strain GM48 (obtained from the ATCC) was admixed with 77λ of deionized water; 2λ of Primer 488 (64 pmoles); and 4λ of primer 489 (56 pmoles). This was followed by a denaturation step (94°C, 5 min.) and a renaturation step (54°C, 5 min.).

30

Thereafter, 4λ of 5 mn dNTPS (Promega, Madison, WI: dATP, Prod. No. U1201; dCTP, Prod. No. U1221; dGTP, Prod. No. U1211; dTTP, Prod. No. U1231), 1λ of Pfu DNA polymerase (Stratagene, La Jolla, CA Prod. No. 600135, 2.5 U/ml), and 50λ of mineral oil overlay was added thereto, followed by 30 cycles, with each

cycle comprising the following: 72°C, 2 min.; 94°C, 1 min.; 54°C, 1 min. Ten microliters (10 λ) of this admixture was analyzed by agarose gel electrophoresis (results not shown); a single band was found at about 400 base pairs.

- 5 The PCR product and the vector were prepared for ligation as follows: Anti-CD20 in ANEX 1 plasmid grown in *E. coli* bacterial strain GM48 was digested with Cla 1 and Xho 1 as follows: 20 λ of anti-CD20 in ANEX 1 was admixed with 10 λ of 10XNEB4 buffer (New England Biolabs, Beverly, MA; hereinafter, NEB); 5 λ Cla 1 (NEB, Prod. No. 197 S, 60u); and 64 λ deionized water. This admixture
- 10 incubated overnight at 37°C, followed by the addition of 5 λ Xho 1 (NEB, Prod. No. 146 S, 100 u) and incubation at 37°C for 2 hrs. The resulting material is designated herein as "Cla 1/Xho 1 cut ANEX 1". The approximate 400 base pair PCR fragment was prepared and digested with Cla 1 and Xho 1 as follows: 90 λ of the PCR fragment was admixed with 10 λ of 3M NaOAc; 1 λ 10% sodium dodecyl
- 15 sulfate (SDS); and 90 λ phenyl/CHCl₃/isoamyl. This admixture was vortexed for 30 sec. followed by a 1 min. spin (1700 RPM). The aqueous phase was subjected to a spin column which resulted in 85 λ total admixture. To this admixture was added 10 λ 10XNEB4, 1 λ bovine serum albumin (BSA, 100X; NEB), 2 λ Cla 1 (24u), and 2 λ Xho 1 (40 u). This admixture was incubated at 37°C for 2 hrs. The
- 20 resulting material is designated herein as "Cla 1/Xho 1 cut PCR 488/489". Both Cla 1/Xho 1 cut ANEX 1 and Cla 1/Xho 1 cut PCR 488/489 were analyzed by agarose gel electrophoresis and the resulting bands were observed at the same relative location on the gel (results not shown).
- 25 Ligation of Cla 1/Xho 1 cut PCR 488/489 and Cla 1/Xho 1 cut ANEX 1 was accomplished as follows: 1 λ of tRNA (Sigma, St. Louis, MO, Prod. No. R-8508) was admixed with 1 λ 10% SDS; 10 λ 3M NaOAc; 45 λ of Cla 1/Xho 1 cut PCR 488/489 (about 22.5 ng); a 1:4 dilution (0.25 λ) of Cla 1/Xho 1 cut ANEX 1 (about 32 ng) in 0.75 λ tris-hydroxymethyl aminomethane ethylenediamine tetracetic

acid (TE); and 42 λ TE. To this admixture was added 90 λ phenyl/CHCl₃/isoamyl, followed by a 30 s c. vortex and a 1 min. spin (1700 RPM). The aqueous phase was transferred to a new tube, followed by addition of 270 λ of 100% EtOH (-20° C), 10 min. spin (12,000 RPM) followed by addition of another 270 λ of 100% EtOH (-20° C) and another 1 min. spin (13,000 RPM). This admixture was dried in a SpeedVAC™ and resuspended in 17 λ TE, 2 λ ligase buffer (Promega, T4 DNA Ligase kit, Prod. No. M180) and 1 λ ligase (Promega Ligase kit). This ligation mix incubated at 14°C overnight. Twenty microliters (20 λ) of the ligation mix was admixed with 10 λ 3M NaOAc, 1 λ 10% SDS, 69 λ TE, and 90 λ phenyl/CHCl₃/isoamyl. This admixture was vortexed for 30 sec., followed by a 1 min. spin (1700 RPM). The aqueous phase was transferred to a new tube and 270 λ of 100% EtOH (-20°C) was added thereto, followed by a 10 min. spin (1700 RPM). This admixture was dried in a SpeedVAC™ and resuspended in 20 λ TE. Ten microliters of the resuspended admixture was transformed in *E. coli* X-L1 blue™ (Stratagene, La Jolla, CA), following manufacturer instructions. Ten (10) bacterial colonies were inoculated in LB Broth (Gibco BRL, Grand Island, NY, Prod. No. M27950B) including ampicillin (50 μ g/ml; Sigma, Prod. No. A-9393). Plasmids were isolated from the 10 cultures with a Promega DNA purification System (Prod. No. PR-A7100), following manufacturer instructions; these plasmids may have comprised the ANEX 2 vector, depending on the sufficiency of the foregoing.

ANEX 2 includes a Hinf I site ("GAATC") upstream of the *neo* start site (-9 to -13 relative to the *neo* start codon); ANEX 1 does not include this Hinf I site. The purified plasmids comprising putative ANEX 2, and previously purified ANEX 1 standard, were subjected to Hinf I digestion as follows: 2 λ of each isolate was admixed with 8 λ of Hinf I digestion buffer (15 λ 10 x NEB2 buffer, 15 λ Hinf I (NEB, Prod. No. 155S, 10u λ); and 90 λ H₂O). This admixture incubated for 3 hrs. at 37°C and each isolate was analyzed via agarose gel electrophoresis

(results not shown); nine (9) of the bands were substantially identical to the ANEX 1 standard, one(1) showed a slight difference in band pattern. For this single isolate, the first two bands were at 1691 and 670 kbp; for the ANEX 1 Hinf I digested product, the first three bands were at 1691, 766, and 670 kbp. The missing band at 766 kbp for the single isolate was attributed to the presence of the Hinf I site therein, indicating that the desired change to ANEX 1 was incorporated into this vector. This vector was designated "Anti-CD20 in ANEX 2 (G1,K)," and is generally referred to by the inventor as ANEX 2.

Electroporation of anti-CD20 in ANEX 2 was accomplished as follows: two-hundred and forty microliters (240 μ l) of the anti-CD20 in ANEX 2 DNA (400 μ g) was admixed with 100 μ l of 10 X NEB2 buffer; 100 μ l of Stu I (NEB, Prod. No. 187S, 1000 u); and 560 μ l TE, and incubated at 37°C for 2hrs. This admixture was then placed over 8 spin columns (125 μ l each), followed by addition of 110 μ l 10X Not I buffer (NEB); 10 μ l 100X BSA; and 20 μ l of Not I (NEB, Prod. No. 189S, 800u). This admixture was incubated at 37°C for 3 hrs., followed by the addition of 120 μ l of 3M NaOAc and 12 μ l of 10% SDS. The admixture was transferred to 2 vortex tubes and 500 μ l of phenyl/CHCl₃/isoamyl was added to each, followed by a 30 sec. vortex and 1 min. spin (1700 RPM). The aqueous phase was removed from the tubes and segregated into 3 tubes, followed by the addition to each tube of -20°C 100% ETOH, followed by 10 min. spin (13,000 RPM). Thereafter, -20°C 70% ETOH was added to each tube, followed by 1 min. spin (13,000 RPM). The tubes were then placed in a Speed VAC™ for drying, followed by resuspension of the contents in 100 μ l TE in a sterile hood. Five microliters (5 μ l) of the resuspended DNA was admixed with 995 μ l of deionized water (1:200 dilution). An optical density reading was taken (OD=260) and the amount of DNA present was calculated to be 0.75 μ g/ μ l. In order to utilize 25 μ g of DNA for electroporation, 32 μ l of the 1:200 dilution of the DNA was utilized (25 μ g was utilized as this was the amount of DNA utilized for TCAE 5.2 and ANEX 1 in the

foregoing Example 1). The 1:200 dilution of DNA was formally referred to as "Stu 1, Not I cut anti-CD20 in ANEX 2 (25µg) in TE" and generally referred to as "anti-CD20 in ANEX 2."

- 5 Host cells utilized was DG44 CHO ("CHO") (see, Urlaub, G. *Somatic Cell*, 1986 *supra*). One hundred milliliters of 6.6×10^5 cells/ml (84%) were subjected to a 2 min. spin at 1000 RPM. These were washed with 50 ml sucrose buffered solution, followed by 5 min. spin at 1000 RPM; the material was then resuspended in 4.5 ml of the sucrose buffered solution. Thereafter, cells were
- 10 counted and 0.4 ml of CHO cells (4.0×10^6 cells) were admixed with 32λ of the anti-CD20 in ANEX 2 in BTX sterile, disposable electroporation cuvettes. Electroporation settings were as follows: 210 volts; 400 microfaraday capacitance; 13 ohms resistance, using a BTX 600™ electro cell manipulator (BTX, San Diego, CA). Nine (9) electroporations were conducted; actual voltage
- 15 delivered over actual times were as follows: 1-199V, 4.23 msec; 2-188V, 4.57 msec; 3-189V, 4.24 msec, 4-200V, 4.26 msec, 5-200V, 4.26 msec; 6-199V, 4.26 msec; 7-189V, 4.59 msec; 8-189V, 4.57 msec; 9-201 V, 4.24 msec. (As noted in Example I, the difference in number of performed electroporations was attributed to the need to achieve a statistically significant number of viable
- 20 colonies for each of the three conditions, TCAE 5.2, ANEX 1 and ANEX 2; the amount of DNA used for each electroporation (25 µg) was the same for each, and the same number of cells were electroporated.

- Thereafter, the electroporation material was admixed with 20 ml of G418
- 25 Growth Media (CHO-S-SFM II minus hypoxanthine and thymidine (Gibco, Grand Island, NT, Form No. 91-0456PK) including 50 µM hypoxanthine and 8 µM thymidine). The admixture was gently agitated, followed by plating 200 µl of the admixture per well into 96-well plates, one plate for each electroporation (nine). Beginning on day 2 after electroporation, through day 17, 150µl of each

well was removed, and 150 μ l of fresh G418 Growth Media containing 400 μ g/ml G418 was added thereto. Colonies were analyzed on day 25.

One hundred and twenty one (121) colonies expressed anti-CD20 antibody (*ie*, 13 colonies per electroporation). Of these, 63 (52%) expressed over 250 μ g/ml of protein; of the 63, 20 of the colonies (16.5%) expressed over 1000 μ g/ml of protein. Only 5 of the 121 colonies (4.1%) expressed less than 25 μ g/ml of protein. Figure 5 provides a histogram comparing expression of protein per colonies derived from the vectors TCAE 5.2, ANEX 1 and ANEX 2.

10

The foregoing data indicates that, *inter alia*, as between ANEX 1 and ANEX 2, the use of at least one out-of-frame start codon upstream of a fully impaired consensus Kozak associated with the translation initiation of a dominant selectable marker decreases the number of viable colonies expressing co-linked gene product and significantly increases the amount of expressed co-linked gene product.

15

20 III. IMPACT OF INSERTION OF GENE PRODUCT OF INTEREST WITHIN AT LEAST ONE ARTIFICIAL INTRONIC INSERTION REGION OF A DOMINANT SELECTABLE MARKER

Building further upon the ANEX 2 vector, an artificial splice was generated between amino acid residues 51 and 52 of the NEO coding region of ANEX 2, followed by insertion therein of the anti-CD20 encoding region. Two such vectors were generated: the first, comprising a consensus Kozak sequence for the NEO translation initiation codon and not comprising an out-of-frame start codon, is referred to as "GKNEOSPLA3F;" the second, comprising a fully impaired consensus Kozak and an out-of frame start condon, is referred to as "NEOSPLA3F."

30

Both GKNEOSPLA3F and NEOSPLA3F contain the following artificial intron sequence between amino acid residues 51 and 52 of NEO:

51 52
5'-CTG CAG/GTAAGT GCGGCGGC TACTAAC (TC)₃ CT (C)₃ TCC (T)₅ C CTGCAG/GAC GAG 3'

The underlined portion represents a sequence amenable to digestion with Not I enzyme; the encoding region for anti-CD20, *inter alia*, was inserted within this region.

10 Although not wishing to be bound by any particular theory, the inventor postulates that during expression, the inclusion of a gene product of interest within an artificial intronic insertion region of a dominant selectable marker (*e.g.* the NEO gene) should significantly decrease the number of viable colonies producing, in the case of the disclosed GKNEOSPA3F and NEOSPLA3F vectors, anti-CD20 antibody. This is predicated upon two points: first, only those vectors
15 which are able to transcribe and correctly splice-out the antibody encoding region and correctly translate NEO will be G418 resistant; second, because each antibody cassette has its own promoter and polyadenylation region, transcription and translation of the antibody is independent of translation of NEO.

20 The GKNEOSPLA3F and NEOSPLA3F vectors were constructed in the following manner:

Anti-CD20 in ANEX 2 was digested with Not I and Xho I in order to isolate the
25 1503 bp NEO cassette DNA fragment (see Figure 4 between "Not I 7023" and
"Xho I 5520") as follows: 10 μ l of anti-CD20 in ANEX 2 was admixed with 6 μ l
deionized H₂O ("dH₂O"); 1 μ l Not I enzyme (NEB, Prod. No. 189S); 2 μ l of 10X
Not I digestion buffer (NEB; provided with enzyme); and 1 μ l Xho I enzyme
(Promega, Madison, WI, Prod. No. R4164). This digestion mixture was
30 incubated overnight at 37°C. The resulting digested DNA was size fractionated

by 0.8% agarose gel electrophoresis and the desired fragment migrating at 1503 was isolated via the GlassMAX™ method (Gibco BRL, Grand Island, NY, Prod. No. 15590-011) for insertion into pBluescript SK(-) plasmid DNA (Stratagene, La Jolla, CA).

5

pBluescript SK (-) was previously prepared for acceptance of the NEO cassette by double digestion with Not I and Xho I using the same conditions as above for anti-CD20 in ANEX 2. Digested pBluescript SK (-) was then collected by ethanol precipitation by the addition of 70 µl dH₂O; 2 µl tRNA (Sigma, St. Louis, MO, Prod. No. R-8508); 10 µl of 3M NaOAc; and 300 µl 100% ETOH (-20°C). This was followed by a 10 min spin (13,000 RPM), decanting the supernatant, rinsing with 70% ETOH, decanting the liquid, drying in a SpeedVAC™ and resuspending in 20 µl 1 x TE.

15 Ligation of the NEO cassette DNA fragment into prepared pBluescript SK (-) vector was accomplished as follows: 10 µl of NEO fragment DNA was admixed with 6 µl dH₂O; 1 µl cut pBluescript SK (-) vector DNA; 2 µl 10 x ligation buffer (Promega, supplied with enzyme); and 1 µl T-4 DNA Ligase (Promega, Prod. No. M1801) followed by incubation at 14°C overnight. Ligated DNA was collected by ethanol precipitation as described above for the preparation of pBluescript SK (-) vector DNA.

25 Ten (10) µl of the resuspended ligated DNA was transformed into *E. coli* XL-1 Blue™ (Stratagene), following manufacturer instructions. Ten (10) bacterial colonies were inoculated in LB broth (Gibco BRL, Prod. No. M27950B) including ampicillin (50 µg/ml; Sigma, Prod. No. A-9393). Plasmids were isolated from the 10 cultures with a Promega DNA purification system (Prod. No. PR-A7100), following manufacturer instructions; these plasmids may have comprised the

plasmid referred to as BlueNEO+ depending on the sufficiency of the foregoing.
(BlueNEO+ was confirmed due to the sufficiency of the following procedure.)

BlueNEO+ contains a Not I restriction recognition sequence reformed upon
5 ligation of the NEO cassette fragment DNA into the pBluescript SK (-) vector.
This site was destroyed by the following: 1 µl of BlueNEO+ DNA was admixed
with 16 µl dH₂O; 2 µl 10 x Not I digestion buffer (NEB); 1 µl Not I enzyme (NEB).
This was followed by incubation at 37°C for 2 hrs. This digested DNA was then
purified by spin column fractionation resulting in 15 µl final volume. This 15 µl
10 Not I digested DNA was "blunt-ended" by admixing with 4 µl 5X Klenow buffer
(20 mM Tris-HCL, pH 8.0, 100mM MgCl₂) and 1 µl DNA Polymerase I Large
(Klenow) Fragment (Promega, Prod. No. M2201). This admixture was incubated
at room temperature for 30 minutes. Blunt-ended DNA was then purified by
spin column fractionation, giving a final volume of 15 µl.

15

Ligation of the blunt-ended DNA was performed in an analogous way as to the
ligation of the NEO cassette fragment DNA into the pBluescript SK (-) vector
except that the final DNA was resuspended in 17 µl of 1 X TE.

20 Following ligation, the DNA was subjected to a second restriction digestion with
Not I by mixing the 17 µl of DNA with 2 µl 10 X Not I digestion buffer and 1 µl
Not I enzyme (NEB). Digestion was allowed to proceed at 37°C for 60 minutes.
Following digestion, the admixture was purified by spin column fractionation
resulting in 15 µl final volume.

25

Ten (10) µl of the purified DNA was transformed into *E. coli* XL-1 Blue™
(Stratagene), following manufacturer instructions. Ten (10) bacterial colonies
were inoculated in LB broth (Gibco BRL including ampicillin (50 µg/ml; Sigma).
Plasmids were isolated from the 10 cultures with a Promega DNA purification

system following manufacturer instructions; these plasmids may have comprised the plasmid referred to as BlueNEO- depending on the sufficiency of the foregoing. (BlueNEO- was confirmed due to the sufficiency of the following procedure.)

5

BlueNEO- contains a unique Pst I restriction site spanning the codons for amino acid residues 51 and 52. BlueNEO- was digested with Pst I as follows: an admixture was formed containing 15 µl dH₂O; 1 µl BlueNEO- DNA, 2 µl digestion buffer 3 (NEB) and 2 µl Pst I enzyme (NEB, Prod. No. 140S). This admixture was incubate at 37°C for 3 hrs. Digested DNA was then purified by spin column fractionation. The following synthetic oligonucleotide was then ligated to the Pst I cohesive ends of BlueNEO-:

5' GGTAAGTGGCGCCGCTACTAACTCTCTCCTCCCTCTTTTCCTGCA 3' (SEQ ID NO: 12) and its complementary sequence:

15 5'GGAAAAAGGAGCGGAGAGAGAGTTAGTAGCGGCCGCACTTACCTGCA 3' (SEQ ID NO: 13).

Insertion of this linker creates a consensus 5' splice donor site (by ligation) followed by a Not I site, followed by a consensus splice branch point, followed by a synthetic polypyrimidine tract, followed by a consensus 3' splice acceptor site, as indicated above.

20

Ligation was performed as described above for the ligation of the NEO cassette into pBluescript SK (-) except using 2 µl of Pst I linearized BlueNEO- DNA and 14 µl (175 pmoles) of annealed complementary oligonucleotides.

25 The foregoing (and following) synthetic oligo nucleotides were chemically synthesized using an Applied Biosystems 391 PCR MATE™ DNA Synthesizer (Applied Biosystems, Foster City, CA). All reagents for the synthesis were purchased from Applied Biosystems.

Ligated DNA was collected by ethanol precipitation as described above for the preparation of pBluescript SK (-) vector DNA.

- 5 Ten (10) μ l of the resuspended ligated DNA was transformed into *E. coli* XL-1 Blue™ (Stratagene), following manufacturer instructions. Ten (10) bacterial colonies were inoculated in LB broth (Gibco BRL) including ampicillin (50 μ g/ml; Sigma). Plasmids were isolated from the 10 cultures with a Promega DNA purification system, following manufacturer instructions; these plasmids may have comprised the plasmid referred to as NEOSPLA and/or NEOSPLA-
10 depending on the sufficiency of the foregoing and the orientation of the insertion of the oligonucleotides.

- Determination of orientation of the splice junction linker was performed by nucleic acid sequencing using the Sequenase Version 2.0 DNA Sequencing Kit
15 (United States Biochemical, Cleveland, OH, Prod. No. 70770) following manufacturer instructions. Upon determination of linker orientation within six independent plasmid isolates, identification of NEOSPLA was made such that the inserted splice junction sequences are in the correct forward orientation with respect to the direction of NEO transcription.

- 20 NEOSPLA was digested with Xho I by forming an admixture of 15 μ l dH₂O; 1 μ l NEOSPLA DNA; 2 μ l 10 X digestion buffer D (Promega, supplied with enzyme); and 2 μ l Xho I enzyme (Promega, Prod. No. R6161). This admixture was digested at 37°C for 3hrs followed by DNA purification by spin column
25 fractionation. Into this site was ligated a self complementary synthetic oligonucleotide having the following sequence: 5' TCGATTAATTAA 3' (SEQ ID NO: 14). Insertion of this sequence effectively changes the Xho I site to a Pac I restriction site (as underlined in SEQ ID NO: 14).

Ligation was performed as described above for the ligation of the NEO cassette into pBlu script SK (-) except using 2 µl of Xho I linearized NEOSPLA DNA and 14 µl (175 pmoles) of annealed complementary oligonucleotides.

- 5 Ligated DNA was collected by ethanol precipitation as described above for the preparation of pBluescript SK (-) vector DNA.

- Ten (10) µl of the resuspended ligated DNA was transformed into *E. coli* XL-1 Blue™ (Stratagene), following manufacturer instructions. Ten (10) bacterial colonies were inoculated in LB broth (Gibco BRL) including ampicillin (50 µg/ml; Sigma). Plasmids were isolated from the 10 cultures with a Promega DNA purification system, following manufacturer instructions; these plasmids may have comprised the plasmid referred to as NEOSPLA3 depending on the sufficiency of the foregoing. (NEOSPLA3 was confirmed due to the sufficiency of the following procedure.)
- 15

- Anti-CD20 in ANEX 2(G1,K) contains the anti-CD20 light chain and heavy chain immunoglobulin cassettes and a DHFR cassette bounded by a Not I site at the 5' end and an Xho I site at the 3' end. Anti-CD20 in ANEX 2(G1,K) was digested with Xho I by forming an admixture of 15 µl dH₂O, 1 µl anti-CD20 in ANEX 2(G1,K) DNA, 2 µl 10 X digestion buffer D (Promega, supplied with enzyme) and 2 µl Xho I enzyme (Promega, Prod. No. R6161). This admixture was digested at 37°C for 3 hrs followed by DNA purification by spin column fractionation. Into this site was ligated a self complementary synthetic oligonucleotide of the following sequence: 5' TCGAAGCGGCGGCT 3' (SEQ ID NO: 15). Insertion of this sequence effectively changes the Xho I site to a Not I restriction site (as underlined in SEQ ID NO: 15).
- 20
- 25

Ligation was performed as described above for the ligation of the NEO cassette into pBluescript SK (-) except using 2 µl of Xho I linearized anti-CD20 in ANEX 2 DNA and 14 µl (175 pmoles) of annealed complementary oligonucleotides.

- 5 Ligated DNA was collected by ethanol precipitation as described above for the preparation of pBluescript SK (-) vector DNA.

- Ten (10) µl of the resuspended ligated DNA was transformed into *E. coli* XL-1 Blue™ (Stratagene), following manufacturer instructions. Ten (10) bacterial colonies were inoculated in LB broth (Gibco BRL, Prod. No. M27950B) including ampicillin (50 µg/ml; Sigma, Prod. No. A-9393). Plasmids were isolated from the 10 cultures with a Promega DNA purification system (Prod. No. PR-A7100), following manufacturer instructions; these plasmids may have comprised the plasmid referred to as Anti-CD20 in ANEX 2(G1,K)A depending on the sufficiency of the foregoing. (This was confirmed due to the sufficiency of the following procedure.)

- Anti-CD20 in ANEX 2(G1,K)A was digested with Not I and Xho I by forming an admixture of 6 µl dH₂O; 10 µl Anti-CD20 in ANEX 2(G1,K); 2 µl 10 x Not I digestion buffer (NEB, supplied with Not I enzyme); and 1 µl Not I enzyme (NEB). This admixture was digested at 37°C for 3 hrs followed by size fractionation by 0.8% agarose gel electrophoresis and the desired fragment migrating at 5515 base pairs by was isolated via the GlassMAX method for insertion into NEOSPLA3.

25

NEOSPLA3 was previously prepared for acceptance of the anti-CD20 cassette by digestion of 1 µl of DNA with Not I using an admixture comprising 16 µl dH₂O;

2 µl 10X Not I digestion buffer (NEB); 1 µl Not I enzyme (NEB); followed by incubation at 37°C for 2 hrs. This digested DNA was then purified by spin column fractionation resulting in 15 µl final volume.

- 5 Ligation of the anti-CD20 DNA fragment into prepared NEOSPLA3 vector was accomplished as follows: 10 µl of anti-CD20 fragment DNA was admixed with 6 µl dH₂O; 1 µl cut NEOSPLA3 vector DNA; 2 µl 10 x ligation buffer (Promega supplied with enzyme); and 1 µl T-4 DNA Ligase (Promega); followed by incubation at 14°C overnight. Ligated DNA was collected by ethanol
10 precipitation as described above for the preparation of pBluescript SK (-) vector DNA.

- Ten (10) µl of the resuspended ligated DNA was transformed into *E. coli* XL-1 Blue™ (Stratagene), following manufacturer instructions. Ten (10) bacterial
15 colonies were inoculated in LB broth (Gibco BRL) including ampicillin (50 µg/ml; Sigma). Plasmids were isolated from the 10 cultures with a Promega DNA purification system following manufacturer instructions; these plasmids may have comprised the plasmids referred to as anti-CD20 in NEOSPLA3F and anti-CD20 in NEOSPLA3R depending on the sufficiency of the foregoing and relative
20 orientation of the inserted fragment with respect to NEO transcription.

- Determination of orientation of the anti-CD20 cassette insertion was preformed by double digestion with KpnI and SpeI (NEB, Prod. No. 1335) in NEB buffer 1 plus acetated BSA as follows: an admixture comprising 4 µl DNA; 2 µl NEB
25 buffer 1; 1 µl Kpn I; 1 µl Spe I; 2 µl BSA; and 10 µl dH₂O was formed. The admixture was digested at 37°C for 2 hrs, followed by size fractionation on an 0.8% agarose gel electrophoresis. Upon determination of anti-CD20 insert orientation within six independent plasmid isolates, identification of anti-CD20

in NEOSPLA3F was made such that the inserted sequences are in the forward orientation with respect to the direction of NEO transcription.

5 The 5515 bp anti-CD20 fragment contains the SV40 origin, a chimeric mouse human immunoglobulin light chain transcriptional cassette, a chimeric mouse human immunoglobulin heavy chain transcriptional cassette, and a murine dihydrofolate reductase transcriptional cassette (see, Figure 4).

10 Anti-CD20 in NEOSPLA3F was doubly digested with Kpn I and Stu I by creating the admixture consisting of 14 µl dH₂O, 1 µl anti-CD20 in NEOSPLA3F, 2 µl 10 x digestion buffer 1 (NEB, supplied with enzyme), 2 µl 10 x acetylated BSA (NEB supplied with Kpn I enzyme), 1 µl Kpn I enzyme, 1 µl Stu I enzyme (NEB, Prod. Nos. 142S and 187S respectively). This admixture was digested at 37°C for 3 hrs followed by size fractionation by 0.8% agarose gel electrophoresis and the desired
15 fragment migrating at 9368 base pairs by was isolated via the GlassMAX method.

A PCR fragment of DNA was generated from TCAE 5.2. The two following synthetic oligonucleotide primers were utilized in the PCR reaction:

20 5' primer: 5' GCA TGC GGT ACC GGA TCC ATC GAG CTA CTA GCT TTG C 3'
(SEQ ID NO: 16);

3' primer: 5' CTG ACT AGG CCT AGA GCG GCC GCA CTT ACC TGC AGT TCA
25 TCC AGG GC 3' (SEQ ID NO: 17)

The underlined portion of SEQ ID NO: 16 represents a Kpn I site, and the underlined portion of SEQ ID NO: 17 represents a Stu I site.

The PCR product was digested with Kpn I and Stu I and then ligated into prepared anti-CD20 in NEOSPLA3F.

5 Ligation of the 627 bp fragment into prepared anti-CD20 in NEOSPLA3F was accomplished as follows:

2 µl anti-CD20 in NEOSPLA3F; 1 µl SDS; 1 µl tRNA (Sigma); 11 µl 3M sodium acetate (pH 4.5) were admixed. Following phenol/chloroform isoamyl extraction of the admixture, the DNA was precipitated from the aqueous phase by addition
10 of 270 µl ethanol (ice-cold) and this was spun at 13,000 rpm for 10 min. Following a 70% ETOH wash, the DNA was resuspended in 16 µl TE, 10 µl of PCR fragment DNA was admixed with 6 µl dH₂O, 1 µl cut anti-CD20 in NEOSPLA3F vector DNA, 2 µl 10 x ligation buffer (Promega, supplied with enzyme) and 1 µl T-4 DNA Ligase (Promega) followed by incubation at 14°C
15 overnight. Ligated DNA was collected by ethanol precipitation as described above for the preparation of pBluescript SK (-) vector DNA.

Ten (10) µl of the resuspended ligated DNA was transformed into *E. coli* XL-1 Blue™ (Stratagene), following manufacturer instructions. Ten (10) bacterial
20 colonies were inoculated in LB broth (Gibco BRL, Prod. No. M27950B) including ampicillin (50 µg/ml; Sigma, Prod. No. A-9393). Plasmids were isolated from the 10 cultures with a Promega DNA purification system (Prod. No. PR-A7100), following manufacturer instructions; these plasmids may have comprised the plasmid referred to as anti-CD20 in GKNEOSPLA3F depending on the
25 sufficiency of the foregoing. (Confirmation was based upon sequence determination of the different regions of GKNEOSPLA3F vs. NEOSPLA3F.)

The new plasmid differs from anti-CD20 in NEOSPLA3F in its Kozak sequence for the NEO gene which is:

-3 +1
 TGT GTT GGG AGC TTG GAT CGAT cc Acc ATG Gtt
 Cla I Start NEO

5 for Anti-CD20 in GKNEOSPLA3F, and

-3 +1
 10 TGT G CCA GCA TGG AGG AAT CGA Tcc Tcc ATG Ctt
 upstream Start Start NEO

for Anti-CD20 in NEOSPLA3F.

15

Comparative analysis of expression of anti-CD20 in TCAE 5 vector (comprising NEO with consensus Kozak); ANEX 2 vector (comprising NEO with fully impaired Kozak, and upstream out-of-frame start sequence); NEOPLA3F (anti-CD20 inserted via artificial intronic insertion region between amino acids 51 and 52 of NEO; NEO has fully impaired Kozak and an upstream out-of-frame start sequence); and GKNEOSPLA3F (anti-CD20 inserted via artificial intronic insertion region between amino acids 51 and 52 of NEO; NEO has consensus Kozak).

20

25 Twenty-five (25) µg of each plasmid (digested as follows: anti-CD20 in TCAE5 and ANEX2 - Not I; anti-CD20 in NEOSPLA3F - Pac I; anti-CD20 in GKNEOSPLA3F - Pac I and Kpn I) was electroporated into 4 x 10⁶ CHO cells; these digestions were utilized to separate the genes expressed in mammalian cells from the DNA used to grow the plasmid in bacteria. Following digestion, EtOH precipitation of the DNA, and drying thereof, the DNA was resuspended in sterile TE at a concentration of 1 µg/µl. Electroporation conditions were as described in Example II, except that 230 volts was utilized and, following electroporation, the mixture of cells and DNA was maintained for 10 min. at room temperature in the sterile, disposable electroporation cuvette.

30

Following electroporation, cells were plated into 96 well dishes as shown below in Table I, based upon the expected frequency of G418 resistant colonies (as derived from preliminary experiments; data not shown):

5

TABLE I
COMPARATIVE EXPRESSION

Plasmid	No. Transfections	No. Cells Plated	No. 96 Well Plates
TCAE 5	1	4×10^5	5
ANEX 2	1	2×10^6	5
GKNEOSPLA3F	1	2×10^6	5
NEOSPLA3F	5	2×10^7	5

10

TABLE 1 (continued)

Plasmid	No. G418 Resistant Colonies	Frequency of G418 Resistant Colony per Transfected Cell
TCAE 5	16	1 in 20,000
ANEX 2	16	1 in 100,000
GKNEOSPLA3F	16	1 in 100,000
NEOSPLA3F	16	1 in 1,000,000

(Cells were fed with G418 containing media on days 2, 5, 7, 9, 12, 14, 18, 22, 26, 30 and 34; supernatant from colonies was assayed for immunoglobulin

15 production and the colonies became confluent in the wells on days 18, 22, 26, 30 and 34).

Figures 7A to 7C provide histogram results and evidence the percentage of colonies at a particular level of expression.

The Examples provided herein are not to be construed as limited to the specific
5 vectors, fully impaired consensus Kozak sequences, dominant selectable
markers, transcriptional cassettes, and/or expressed proteins. The fully
impaired consensus Kozak, and the utilization thereof, are not to be construed as
limited to ANEX 1 and ANEX 2 vectors. Similarly, the preferred fully impaired
consensus Kozak sequences and vectors in no way constitute an admission,
10 either actual or implied, that these are the only sequences or vectors to which the
inventor is entitled. The inventor is entitled to the full breadth of protection
under applicable patent laws. Preferred vectors incorporating fully impaired
consensus Kozak sequences have been identified by the inventor on ANEX 1 and
ANEX 2 for purposes of claiming these vectors by designating plasmids
15 comprising these vectors and anti-CD20 were deposited with the American Type
Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland, 20852,
under the provisions of the Budapest Treaty for the International Recognition of
the Deposit of Microorganisms for the Purpose of Patent Procedure. The
plasmids were tested by the ATCC on November 9, 1992, and determined to be
20 viable on that date. The ATCC has assigned these plasmids the following ATCC
deposit numbers 69120 (anti-CD20 in TCAE 12(ANEX 1)) and 69118 (anti-CD20
in ANEX 2 (G1,K)); for purposes of this deposit, these plasmids were transformed
into *E. coli*.

25 Although the invention has been described in considerable detail with regard to
certain preferred embodiments thereof, other embodiments within the scope of
the teachings of the present invention are possible. Accordingly, neither the
disclosure nor the claims to follow, are intended, nor should be construed to be,
limited by the descriptions of the preferred embodiments contained here.

SEQUENCE LISTING

(1) GENERAL INFORMATION

- 5 (i) APPLICANT: Reff, Mitchell E.
- 10 (ii) TITLE OF INVENTION: Impaired Dominant Selectable Marker
Sequence and Intronic Insertion
Strategies for Enhancement of
Expression of Gene Product and
Expression Vector Systems Comprising
Same
- 15 (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDING ADDRESS:
- 20 (A) ADDRESSEE: IDEC Pharmaceuticals Corporation
(B) STREET: 11011 Torreyana Road
(C) CITY: San Diego
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92121
- 25 (v) COMPUTER READABLE FORM:
- 30 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
(B) COMPUTER: Macintosh
(C) OPERATING SYSTEM: MS.DOS
(D) SOFTWARE: Microsoft Word 5.0
- (vi) CURRENT APPLICATION DATA:
- 35 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- 40 (A) NAME: Burgoon, Richard P. Jr.
(B) REGISTRATION NUMBER: 34,787
(C) REFERENCE/DOCKET NUMBER:
- 45 (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (619) 550-8500
(B) TELEFAX: (619) 550 8750

- (2) INFORMATION FOR SEQ ID NO: 1:
- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 17 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: yes
- 15 (iv) ANTI-SENSE: yes
- (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
- 20 TAG CTA GGT CCT ACC CC 17
- (3) INFORMATION FOR SEQ ID NO: 2:
- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 17 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: yes
- (iv) ANTI-SENSE: no
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
- ATC GAT CCT GGA TGC GG
- 40 (4) INFORMATION FOR SEQ ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
- 45 (A) LENGTH: 9 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: yes
- (iv) ANTI-SENSE: no

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
TNN ATG CTT 9
- 5 (5) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 9 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single, including nick
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: (DNA (genomic)
- (iii) HYPOTHETICAL: yes
- (iv) ANTI-SENSE: no
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
- CNN ATG CTT 9
- 25 (6) INFORMATION FOR SEQ ID NO: 5:
- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 9 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (ii) HYPOTHETICAL: yes
- (iv) ANTI-SENSE: no
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
- TNN ATG TTT 9

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 9 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(ii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: no

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CNN ATG TTT

9

20 (8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 29 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(ii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: no

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TTG GGA GCT TGG ATC GAT
CCA CCA TGG TT

18
11

40 (9) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 29 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

- (ii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
- TTG GGA GCT TGG ATC GAT 18
CCT CCA TGC TT 11
- 10 (10) INFORMATION FOR SEQ ID NO: 9:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 15
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (ii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
- CCA GCA TGG AGG AAT CGA TCC 21
TCC ATG CTT 9
- 30 (11) INFORMATION FOR SEQ ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 35
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- (ii) HYPOTHETICAL: yes
- (iv) ANTI-SENSE: yes
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
- GGA GGA TCG ATT CCT CCA TGC TGG 24
CAC AAC TAT GTC AGA AGC AAA TGT GAG C 28
- 50

(12) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(ii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTG GGG CTC GAG CTT TGC

18

20 (13) INFORMATION FOR SEQ ED NO: 12

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 47 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(ii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no62

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGT AAG TGC GGC CGC TAC TAA CTC TCT CCT
CCC TCC TTT TTC CTG GA

30

17

40 (14) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 47 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

(ii) HYPOTHETICAL: no

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

5 GGA AAA AGG AGG GAG GAG AGA GTT AGT AGC GGC 33
CGC ACT TAC CTG CA 14

(15) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 12 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(ii) HYPOTHETICAL: no

20

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

25 TCG ATT AAT TAA 12

(16) INFORMATION FOR SEQ ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 14 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

(ii) HYPOTHETICAL: no

40

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCG AAG CGG CCG CT 14

45 (17) INFORMATION FOR SEQ ID NO: 16

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

GCA TGC GGT ACC GGA TCC ATC GAG CTA 27
CTA GCT TTG C 10

10 (18) INFORMATION FOR SEQ ID NO: 17

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 47 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(ii) HYPOTHETICAL: no

25 (iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

CTG ACT AGG CCT AGA GCG GCC GCA CTT ACC 30
TGC AGT TCA TCC AGG GC 17

30

CLAIMS

What is claimed is:

- 5 1. An expression vector for expressing a protein of interest by recombinant deoxyribonucleic acid techniques, said vector comprising at least one dominant selectable marker, wherein the translation initiation start site of said marker comprises the following sequence:

10 -3 +1
 Pyxx ATG Pyxx

where "Py" is a pyrimidine nucleotide; "x" is a nucleotide; and the numerical designations are relative to the codon "ATG".

- 15 2. The expression vector of claim 1 wherein the nucleic acid sequence encoding for the protein of interest is co-linked to said dominant selectable marker.
- 20 3. The expression vector of claim 1 wherein said dominant selectable marker is selected from the group consisting of: herpes simplex virus thymidine kinase, adenosine deaminase, asparagine synthetase, *Salmonella* his D gene, xanthine guanine phosphoribosyl transferase, hygromycin B phosphotransferase, and neomycin phosphotransferase.
- 25 4. The expression vector of claim 1 wherein said translation initiation start site sequence is selected from the group consisting of TxxATGCxx; CxxATGCxx; CxxATGTxx; and TxxATGTxx, where "x" is a nucleotide, with the proviso that the codon "Txx" downstream of the ATG codon does not encode a
- 30 stop codon.

5. The expression vector of claim 1 wherein said translation initiation start site sequence is TxxATGCxx, where "x" is a nucleotide.

6. The expression vector of claim 1 wherein said translation initiation
5 start site sequence is TCCATGCTT.

7. The expression vector of claim 1 wherein said translation initiation start site sequence is located within a secondary structure.

10 8. The expression vector of claim 1 wherein said translation initiation start site sequence further comprises at least one out-of-frame start codon within about 1000 nucleotides of the ATG start codon of said start site, with the proviso that no in-frame stop codon is located within said 1000 nucleotides.

15 9. The expression vector of claim 1 wherein said translation initiation start site sequence further comprises at least one out-of-frame start codon within about 350 nucleotides of the ATG start codon of said start site, with the proviso that no in-frame stop codon is located within said 350 nucleotides.

20 10. The expression vector of claim 1 wherein said translation initiation start site sequence further comprises at least one out-of-frame start codon within about 50 nucleotides of the ATG start codon of said start site, with the proviso that no in-frame stop codon is located within said 50 nucleotides.

25 11. The expression vector of claims 8, 9 and 10 wherein said out-of-frame start codon is part of a consensus Kozak sequence.

12. The expression vector of claim 10 wherein said out-of-frame start codon and said translation initiation start site sequence are both included as part of a secondary structure.

5 13. The expression vector of claims 8, 9, 10 wherein said translation initiation start site sequence is part of a secondary structure and said out-of-frame start codon is not part of said secondary structure.

10 14. A dominant selectable marker encoded by a nucleic acid sequence, wherein the translation initiation start site of said dominant selectable marker is selected from the group consisting of TxxATGCxx; CxxATGCxx; CxxATGTxx; and TxxATGTxx, where "x" is a nucleotide, with the proviso that "Txx" downstream of the ATG codon does not encode a stop codon.

15 15. The material of claim 14 wherein said dominant selectable marker is selected from the group consisting of herpes simplex virus thymidine kinase, adenosine deaminase, asparagine synthetase, *Salmonella* his D gene, xanthine guanine phosphoribosyl transferase, hygromycin B phosphotransferase, and neomycin phosphotransferase.

20

16. The material of claim 14 wherein said translation initiation start site sequence is TxxATGCxx, where "x" is a nucleotide.

17. The material of claim 14 wherein said translation initiation start
25 site sequence is TCCATGCTT.

18. The material of claim 14 wherein said translation initiation start site sequence is located within a secondary structure.

19. The material of claim 14 wherein said translation initiation start site sequence further comprises at least one out-of-frame start codon within about 1000 nucleotides of the ATG start codon of said start site, with the proviso that no in-frame stop codon is located within said 1000 nucleotides.

20. The material of claim 14 wherein said translation initiation start site sequence further comprises at least one out-of-frame start codon within about 350 nucleotides of the ATG start codon of said start site, with the proviso that no in-frame stop codon is located within said 350 nucleotides.

21. The material of claim 14 wherein said translation initiation start site sequence further comprises at least one out-of-frame start codon within about 50 nucleotides of the ATG start codon of said start site, with the proviso that no in-frame stop codon is located within said 50 nucleotides.

22. The material of claims 19, 20 and 21 wherein said out-of-frame start codon is part of a consensus Kozak sequence.

23. The material of claim 21 wherein said out-of-frame start codon and said translation initiation start site sequence are both included as part of a secondary structure.

25

24. The material of claims 19, 20, 21 wherein said translation initiation start site sequence is part of a secondary structure and said out-of-frame start codon is not part of said secondary structure.

25. An expression vector selected from the group consisting of ANEX 1 (included within American Type Culture Collection deposit number 69120) and ANEX 2 (included within ATCC deposit number 69118).

5 26. A plasmid comprising the expression vector of claim 1 wherein the nucleic acid sequence encoding for said protein of interest is co-linked to said dominant selectable marker.

10 27. The plasmid of claim 26 integrated within the cellular deoxyribonucleic acid of a mammalian host cell.

15 28. The plasmid of claim 27 wherein said host cell is selected from the group consisting of DG44, DXB11, CV1, COS, R1610, SP2/0, P3x633-Ag8.653, BFA-1c1BPT, RAJI, and 293.

 29. The expression vector of claim 1 further comprising an artificial intronic insertion region within said dominant selectable marker, wherein an encoding sequence for a protein of interest is located within said insertion region.

20 30. The dominant selectable marker of claim 14 further comprising an artificial intronic insertion region.

Neomycin phosphotransferase gene

		Cla I	-3	+1
TCAE 5.2	TTGGGAGCTTGG	<u>ATCGAT</u>	CC	A cc ATG Ctt Met Val
ANEX 1	TTGGGAGCTTGG	<u>ATCGAT</u>	CC	I cc ATG Ctt Met Leu
ANEX 2	CCaGCATGgAGGA	<u>ATCGAT</u>	CC	I cc ATG Ctt Met Leu

FIG. 1

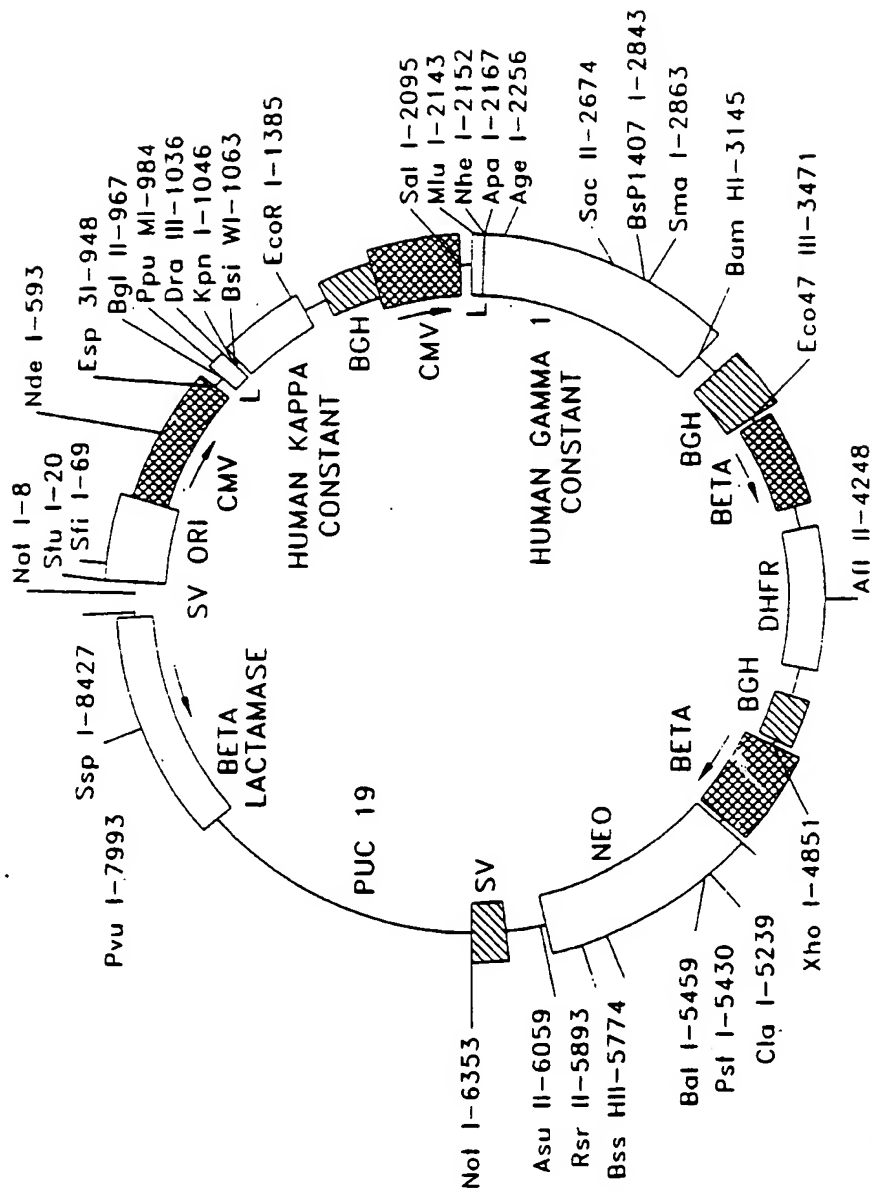
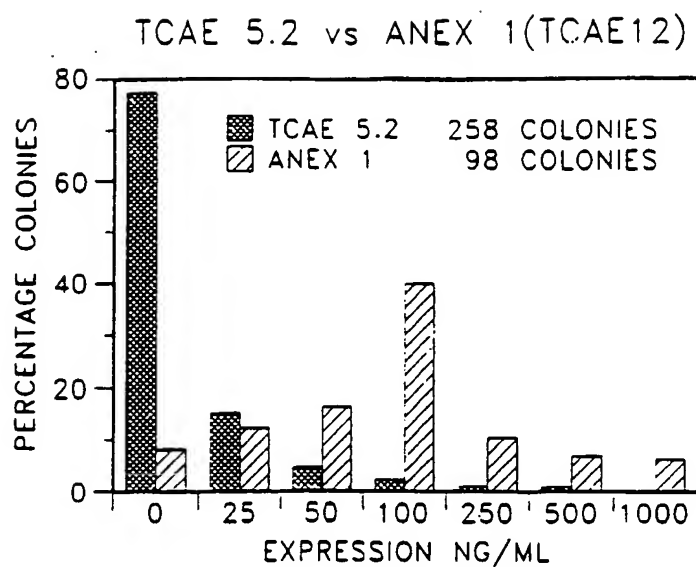
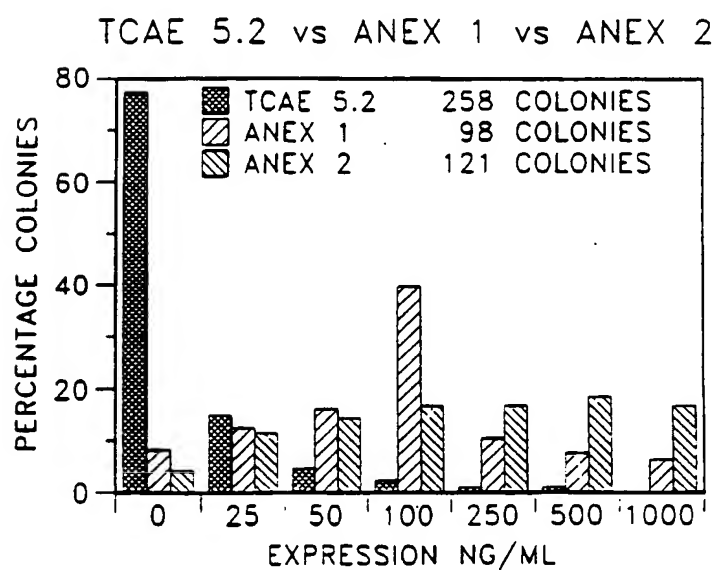


FIG. 2

*FIG. 3**FIG. 5*

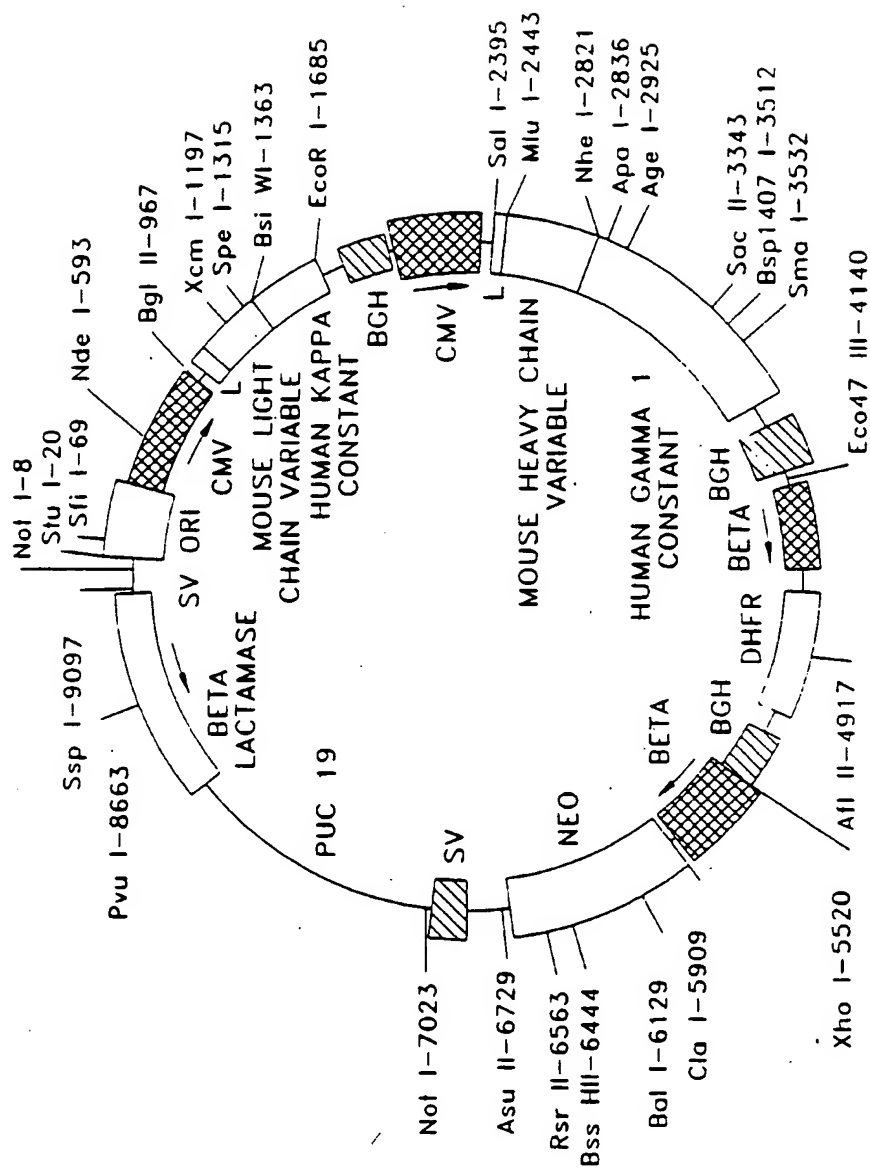


FIG. 4

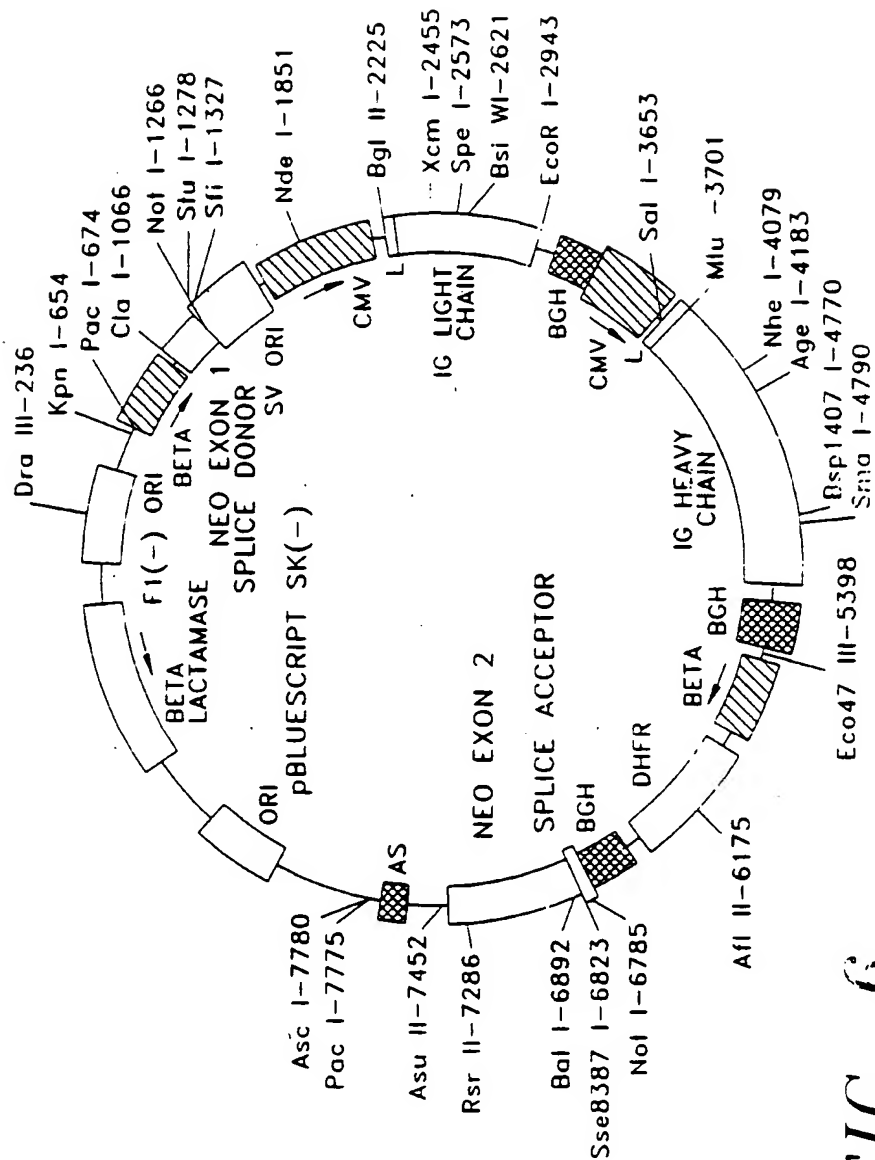


FIG. 6

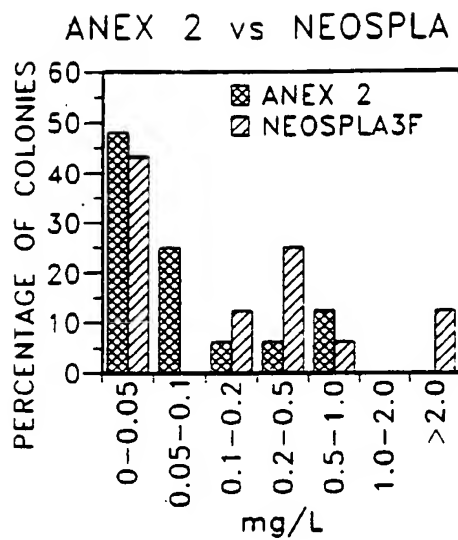


FIG. 7B

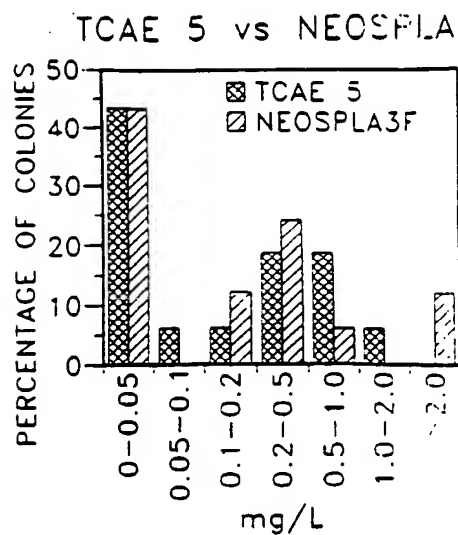


FIG. 7A

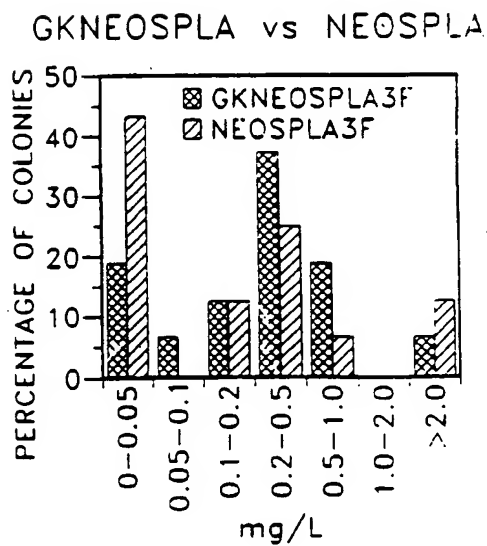


FIG. 7C